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Matches 211; Conservative
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Best Local
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C, Function:
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T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Alathors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A,Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69735
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-213 «KUN»
A;Residues: 1-214 «KUN»
A;Residues: 1-215 «KUN»
A;Residues: 1-215 «KUN»
C;Genetics:
A;Gene: xyna
A;Berences: UNIPARC:UP10000336C9; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CA;Genetics:
A;Gene: xyna
A;Berence: Strain 168
C;Genetics:
A;Gene: xyna
A;Berence: Strain 168
C;Function: Catalyzes the hydrolysis of 1,4-beta-xylanase homology
C;Reynords: extracellular protein; 91ycosidase; hydrolase; polysaccharide degradation
C;Superfamily: endo-1,4-beta-xylanase A #status experimental «MAT»
F;128/Domain: signal sequence #status predicted «Sio»
F;22-213/Pomain: signal sequence #status experimental k;200/Active site: Glu #status predicted
F;200/Active site: Glu #status predicted
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100.0%; Pred. No. 2.4e-80;
ive 0; Mismatches 0;
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Matches 213; Conservative
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NyAlternate names: xylanase S
Cyspecies: Bacillus sp.
A;Variety: strain YA-14
C;Date: 14-Jul-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: S48126
K;Ju-Hyun, Y.; Park, Y.s.; Yum, D.Y.; Kim, J.M.; Kong, I.S.; Bai, D.H.
J. Microbiol. Biotechnol. 3, 139-145, 1993
A;Title: Nucleotide sequence and analysis of a xylanase gene (xynS) from alkali-tolerant
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A;Cross-references: UNIPROT:Q59256; UNIPARC:UPI000060D47; EMBL:X59058; NID:g458800; PID
A;Experimental source: strain YA-14
C;Genetics:
C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase; bydrolase; polygaccharide degradation
C;Keywords: extracellular protein; 91ycosidase; hydrolase; polygaccharide degradation
F;1-28/Domain: signal sequence #status predicted <515>
F;29-213/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F;31-213/Domain: endo-1,4-beta-xylanase homology <XYLD:
F;91.08,140/Binding site: substrate (Tyr, Tyr, Arg) #status experimental
F;106,200/Active site: Glu #status experimental
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C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Superfamily: endo-1,4-beta-xylanase; hydrolase; polysaccharide degradation
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-213/Product: endo-1,4-beta-xylanase S #status predicted <WAT>
F;10-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F;106,200/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
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Pred. No. 6.6e-80;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                             Score 1168; DB 1;
Pred. No. 3.9e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                                                                                                                                                                                                                         Query Match

Best Local Similarity 99.5%;
Matches 212; Conservative 1
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us-10-626-724-5.rpr

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein February 3, 2006, 09:08:23 ; Search time 42 Seconds (without alignments) 487.956 Million cell updates/sec Run on:

US-10-626-724-5 Title: Perfect score:

1171 1 MFKFKKNFLVGLSAALMSIS......YQVMATEGYQSSGSSNVTVW 213 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ΙD	Description
1	1171	100.0	213	п	140569	endo-1,4-beta-xyla
7	1168	99.7	213	Н	S01734	endo-1,4-beta-xyla
3	1165	99.5	213	Ч	S48126	endo-1,4-beta-xyla
4	864.5	73.8	210	~	C83762	endo-1,4-beta-xyla
S	651.5	55.6	241	~	T37005	endo-1,4-beta-xyla
Q	637	54.4	240	Н	JS0591	endo-1,4-beta-xyla
7	621	53.0	240	Ч	847512	4
80	609.5	52.0	644	7	140712	4-
6	9	51.2	225	Н	S57477	4
10	594	50.7	333	7	JS0590	endo-1,4-beta-xyla
11	594	50.7	335	7	T50601	endo-1,4-beta-xyla
12	578	49.4	232	~	JC7577	endo-1,4-beta-xyla
13	577	49.3	221	-	S57469	endo-1,4-beta-xyla
14	552	47.1	227	~	S43919	endo-1,4-beta-xyla
15	540	46.1	219	~	S71472	endo-1,4-beta-xyla
16	530	45.3	197	-	A44597	4
17	525	44.8	221	~	JC7307	endo-1,4-beta-xyla
18	523	44.7	190	٦	A44595	endo-1,4-beta-xyla
19	515.5	44.0	241	~	S71473	endo-1,4-beta-xyla
20	513	43.8	190	٦	A44593	endo-1,4-beta-xyla
21	206	43.2	190	ч	A44594	endo-1,4-beta-xyla
22	505	43.1	223	~	S39883	-beta
23	503	43.0	222	~	S39154	xylanase 1 - fungu
24	480.5	41.0	354	Н	S51779	endo-1,4-beta-xyla
25	469	40.1	661	٦	859633	₹.
26	461.5	39.4	228	-	WWBSXP	endo-1,4-beta-xyla
27	436	37.2	929	Н	S59631	4-
28	420	35.9	261	Н	S12745	endo-1,4-beta-xyla
29	409	34.9	511	-4	JQ1935	endo-1,4-beta-xyla

xylanase 2 - fungu endo-1,4-beta-xyla	endo-1,4-beta-xyla	endo-1,4-beta-xyla	endo-1,4-beta-xyla	endo-1,4-beta-xyla	endo-1,4-beta-xyla	XynB precursor - R	xylanase, beta(1,3	endo-1,4-beta-xyla	endoxylanase - rum	xylanase (EC 3.2.1	endo-1,4-beta-xyla	hypothetical prote	endo-1,4-beta-xyla	lysozyme 2 (EC 3.2
S39155 S20907	JC1198	S48229	S58235	S49542	JC4909	851592	A36910	S24754	849528	B53295	548865	T04776	A61149	A42296
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229 954	211	211	789	211	209	781	802	607	607	809	266	313	20	999
34.6 229 33.1 954														
	32.7		32.2	32.0	30.8	29.8	28.7	23.2	22.6	22.4		11.4	10.8	10.2

## ALIGNMENTS

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	89.		-Jul-2004				in Bacillus			translated f		
	subtili		ange 09				пгутев			shown;		
	lus		t Ch	1711			ng e			not		
	endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Bacillus subtilis		C; Date: 12-Aug-1996 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004	C; Accession: I40569; S39157; S39158; A53635; F69735; S51711	ъ.		A,Title: Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus su	A; Reference number: 140370; MUID:95219081; PMID:7704256		A;Status: nucleic acid sequence not shown; translation not shown; translated fro		
	A precu		ion 02-J	A53635	R;Wolf, M.; Geczi, A.; Simon, O.; Borriss, R.		sta-gluc	119081;		shown;		
	1.8)		eviai	3158;	.; B		od be	3:952		not		
	3.2.	₹ <sub>62</sub>	Ce re	33	o t	1995	an ar	M		ence		Č
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RESULT 1 140569	endo-	NyAlternate names: Xylanase A C;Species: Bacillus subtilis	C; Dat	C; Acc	R; Wol	Microbiology 141, 281-290, 1995	A;Tit	A;Ref	A; Accession: I40569	A;Sta	A; Molecule type: DNA	1001 CTC 10 101 CT 101
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ubtilis:

om GB/EME

A;Residues: 1:-22,'P',24-213 <WOL>
A;Residues: 1:-22,'P',24-213 <WOL>
A;Cross-references: UNIPROT:P18429, UNIPARC:UPI00000B63D0; EMBL:Z34519; NID:g2995396; P1
A;Experimental source: strain 168
B;Paice, M.G.; Bourbonnais, R.; Desrochers, M.; Jurasek, L.; Yaguchi, M.
Arch. Microbiol. 144, 201-206, 1986
A;Title: A xylanase gene from Bacillus subtilis: nucleotide sequence and comparison with A;Reference number: S39157

A;Accession: S39157

A,Residues: 1-213 <PAI1> A,Cross-references: UNIPARC:UP100000336C9, EMBL:M36648; NID:g143842; PIDN:AAA22897.1; P1 A,Experimental source: strain PAP115 A, Molecule type: DNA

A.Accession: 839158
A.Molecule type: protein
A.Residues: 29-58;60-73;75-76 <PAI2>
A.Residues: 29-58;60-73;75-76 <PAI2>
A.Crossa-references: UNIPARC:UP1000015759E; UNIPARC:UP10000172962; UNIPARC:UP10000172963
A.Experimental source: strain PAPI15
A.Experimental source: strain PAPI15
B.Miao, S.; Ziser, L.; Aebersold, R.; Withers, S.G.
Biochemistry 33, 7027-7032, 1994

RiMião, S.; Ziser, L.; Aebersold, R.; Withers, S.G. Bochemistry 33, 7027-7032, 1994 A;Title: Identification of glutamic acid 78 as the active site nucleophile in Bacillus s A;Reference number: A53635; MUID:94271752; PMID:7911679 A;Accession: A53635

A;Status: preliminary

A;Molecule type: protein A;Residues: 97-107 <MIA> A;Cross-references: UNIPARC:UP10000172964

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--- DYWQNWTDGGGIVNAVNGSG

KKNFLVG---LSAALMSISLFSATASAAST---

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TYKGTVKSDGGTYDI YTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA

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A; ACCESSION: J30591
A; Molecule type: DNA
A; Residues: 1-240 <SIRA>
A; Cross-references: UNIPROT: P26220; UNIPARC: UPI0000034D31; GB: M64553; NID: g153530; PIDN
A; ACCESSION: P50240
A; Molecule type: protein
A; Residues: 50-80 <SIR2>
A; Cross-references: UNIPARC: UPI0000172965
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AjGene: Xinc
C;Function:
AjBethway: xinc
A;Pethway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-49/Domain: signal sequence #status predicted <SIG>
F;60-240/Product: endo-1,4-beta-xylanase C #status experimental <MAT>
F;62-239/Domain: endo-1,4-beta-xylanase homology <XXL>
F;125/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 107, 75-82, 1991
A;Title: Sequences of three genes specifying xylanases in Streptomyees lividans.
A;Reference number: JS0589; MUID:92077439; PMID:1743521
                                                                                                                                 GNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVD 1111
                                                                                                                                                                                                                         SWGTYRPIGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNAT 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNAT 171
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C;Species: Streptomyces lividans
C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: JS0591; PS0240
C;Accession: JS0591; PS0240
R;Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
      5 KKNFLVG---LSAALMSISLFSATASAAST------DYWQNWTDGGGIVNAVNGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endo-1,4-beta-xylanase (EC 3.2.1.8) C precursor - Streptomyces lividans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb.
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                                                                                                                                                                                                                                                                                                                                                       172 ITPSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTV 212
                                                                                                                                                                                                                                                                                                                                                                                                ITFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTV
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Matches 127; Conservative
                                                                                           22
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                                                                                                                                                                                                                                                                                                                                             C;Species Bacillus halodurans
C;Species Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete genome sequence of the alkaliphilic bacterium C83762
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83762
A;Accession: C83762
A;Accession: C83762
A;Accession: C83762
A;Coss-references: UNIPROT:Q9KEF3; UNIPARC:UPI0000DCBD1; GB:AP001510; GB:BA000004; NIC
C;Genetics: B10899
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cipecies: Streptomyces coelicolor
cipate: Oslocies: Dslocies: Dslo
                                                                                                                                                                                                                                                                                                                         endo-1,4-beta-xylanhydrolase BH0899 [imported] - Bacillus halodurans (strain C-125)
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59 TGNFVVGKGWEIGSPNRTIHYNAGVWEPSGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
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Best Local Similarity 74.2%; Pred. No. 1.6e-57;
Matches 158; Conservative 19; Mismatches 33
                                                                                                                                 181 WKSHGMNLGSNWAYQVLATEGYQSSGSSNVTVW 213
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Gaps

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Riperez-Gonzalez, J.A.

Riberez-Gonzalez, J.A.

Rubmitted to the EMBL Data Library, June 1995

A; Description: Expression in Saccharomyces cerevisiae of two xylanase encoding genes from the EMBL by the strength of the EMBL strength of the strength of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 NFVVCKCWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRP--TG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 NFVGGKGWNPGST-RTINY-GGSFNPSGNGYLAVYGWTQNPLIEYYIVESYGTYNPGSGG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 QHRGTVYSDGATYDIYTATRYNAPSIEG-TATFEQFWSVRQSKRTGG---TVTTANHFNA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans A; Description: catalyzes the hydrolysis of 1,4-beta-xylanase homology C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-19/Domain: signal sequence #status predicted <SIG>F;1-19/Domain: endo-1,4-beta-xylanase 1 #status predicted <MAT>F;48-225/Product: endo-1,4-beta-xylanase homology <XYL>F;21,212/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: xylanase 1
C;Species: Emericalla nidulans, Aspergillus nidulans
C;Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: S57477
                                                                                                                                                                                                                                                                                                                                                                                          1.7 RPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAAREASLLERSTPSSTG-----WSNGYYYSFWTDGGGDVTYTNGAGGSYTVQWSNVG
                                                                                                                                                                                                                                        20 LTGLLAAGALVAGALAAASPAAAAVTSNTTGTHDGYFYSFWTDSPGSVSMDLNSGGGYT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LVGLSAALMSISLFSATASAASTDYWQN-----WTDGGGIVNAVNGSGGNYSVNWSNTG
                                                                                                                                                                                                                                                                                                                                     57 NWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans N;Alternate names: xylanase B C;Species: Streptomyces lividans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 600; DB 1; Length 225; Pred. No. 8.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Indels
                                                          44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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y 56.8%; Pred. No. e...

'... 29; Mismatches
                                                               Mismatches
                                                                                                                                                      9 LVGLSA--ALMSISLFSATASAASTD----
              Best Local Similarity 57.4%; Pre
Matches 124; Conservative 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 56.89
Matches 121; Conservative
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C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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C;Species: Streptomyces sp.
C;Date: 13-Jan-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: S47512
R;Mazy-Servals, C.; Moreau, A.; Gerard, C.; Dusart, J.
Submitted to the EMBL Data Library, August 1994
A;Description: Cloning and sequencing of a xylanase-encoding gene from Streptomyces sp.
A;Accession: S47512
A;Nolecule type: DNA
A;Residues: 1-240 <AMZ>
A;Accession: S47512
A;Molecule type: DNA
A;Residues: 1-240 <AMZ>
A;Cross-references: UNIPROT:Q56013; UNIPARC:UPI00000421AE; EMBL:X81045; NID:g531767; PIL
A;Experimental source: strain EC3
A;Cross-references: UNIPROT:Q56013; UNIPARC:UPI00000421AE; EMBL:X81045; NID:g531767; PIL
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A;Description: strain EC3
C;Kunction:
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase; hydrolase; polysaccharide degradation
C;Superfamily: endo-1,4-beta-xylanase #status predicted <AMT>
F;62-239/Domain: endo-1,4-beta-xylanase homology <AXL>
F;48-240/Product: endo-1,4-beta-xylanase homology <AXL>
F;135,226/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1407-1, 4-beta-xylanase (EC 3.2.1.8) D precursor - Cellulomonas fimi
N;Alternate names: xylanase D
C;Species: Cellulomonas fimi
C;Species: Cellulomonas fimi
C;Bacesion: I40712
R;Millward-Sadler, S.J.; Poole, D.M.; Henrissat, B.; Hazlewood, G.P.; Clarke, J.H.; Gilb
Mol. Microbiol. 11, 375-382, 1994
A;Title: Evidence for a general role for high-affinity non-catalytic cellulose binding d
A;Accession: I40712
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Genecules: 1-644 cRES>
A;Cross-references: UNIPROT:P54865; UNIPARC:UPI0000139097; EMBL:X76729; NID:g558176; PID
C;Genetion:
A;Genetics:
A;Geneti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 SWGTYRPIGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTPTQYWSVRQSKRPTGSNAT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKNFLVG---LSAALMSISLFSATASAAST------DYWQNWTDGGGIVNAVNGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.0%; Score 621; DB 1; 56.1%; Pred. No. 2.4e-39; iive 26; Mismatches 53.
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Best Local Similarity 56.11
Matches 124; Conservative
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Gaps

22;

62 79

52.0%; Score 609.5;

Query Match

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C;Accession: JC7577; PC7120
R;Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka, Bisoci: Biotechnol. Biochem. 64, 2734-2738, 2000
A;Title: Molecular cloning, overexpression, and purification of a major xylanase from As A;Reference number: JC7577; MUID: 21077500; PMID:11210150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT: P55333; UNIPARC: UPI0000139075; EMBL: Z49893; NID: 9870834; PID C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endoxylanases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    two xylanase encoding genes
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                                                                                                                                                                                  42 GIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 SPLIEYYVVDSWGTYRP--TGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSV 159
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                                                                                                                                                                                                                                                                                                                                                                                      endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
C;Species: Aspergillus oryzae
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
                                       change 09-Jul-2004
                                                                                                                                                 153 FTQYWSVRQSKRPTGSNATITFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SILLACSAAIGALATPIEPLADHPNEAFNETAFNDLVGRSTPSSTGYNNGYYSFWTDGG
       93 YLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 NFLVGLSAALMSIS-----LFSATA-----SAASTD----YWQNWTDGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-232 <KIM>
A;Cross-references: UNIPROT: 09HFA4; UNIPARC: UP10000069976; DDBJ: AB044941
A;Experimental source: strain KBN616
A;Accession: PC7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 ROSKRPTGSNATITFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UP10000175A84
C;Comment: This enzyme has strong similarity to other fungal family 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: xynG2
A;Introns: 100/2
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NiAlternate names: xylanase 2
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 10-oct-1995 #sequence_revision 22-Nov-1996 #text_C;Accession: S57469
R;Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A;Description: Expression in Saccharomyces cerevisiae of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.4%; Score 578; DB 2; 52.1%; Pred. No. 3.8e-36; ive 31; Mismatches 47;
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Matches 122; Conservative 3
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Best Local Similarity
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A; Molecule type: DNA
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A;Molecule type: DNA
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A; Residues: 1-33 <SIR>
A; Residues: 1-33 <SIR>
A; Residues: 1-33 <SIR>
A; Residues: 1-33 <SIR>
A; Accession: PS0239
A; Molecule type: protein
A; Residues: 41-71 <SIR>
A; Molecule type: protein
A; Residues: 41-71 <SIR>
A; Molecule type: protein
A; Residues: 41-71 <SIR>
A; Cross-references: UNIPARC:UPI000017296B
C; Genetics:
A; Genetics:
A; Genetics:
A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A; Description: catalyzes the protein; glycosidase; hydrolase; polysaccharide degradation
C; Superfamily: Clostridium endo-1, 4-beta-xylanase B; endo-1,4-beta-xylanase homology
C; Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F; 14-133/Product: endo-1,4-beta-xylanase B #status experimental <MAT>
F; 54-230/Domain: endo-1,4-beta-xylanase homology <XYL>
F; 127,217/Active site: Glu #status predicted
   C;Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999 C;Accession: JS0590; PS0239 R;Shareck, F:; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D. Gene 107, 75-82, 1991 C;Yaguchi, M.; Morosoli, R.; Kluepfel, D. A;Title: Sequences of three genes specifying xylanases in Streptomyees lividans. A;Reference number: JS0589; MuID:92077439; PMID:1743521 A;Accession: JS0599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 YLALYGWTSNPLVEYYIVDNWGTYRPTGEYKGTVTSDGGTYDIYKTTKVNKPSVEGTR-T 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 FTQYWSVRQSKRPTGSNATITFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Peb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 YWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 YMQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.7%; Score 594; DB 1; Length 333; Best Local Similarity 62.2%; Pred. No. 3.6e-37; Matches 112; Conservative 19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 335;
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llarity 62.2%; Pred. No. 3.6e-37;
Conservative 19; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
112; Conserv
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Matches 111; Conservative
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                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-219 < YOS>
                                                                                                                                                                                                                                                                                               A;Accession: S71472
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                     191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Function:
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                                                                                                                                                                                                                                                                                                                               46 AVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLI 105
                                                                                                                                                                                                                                                                                                                                                   59 YTNGDGGSYTVEWTKVGNFVGGKGWNPGSS-QTISY-SGSFIPSGNGYLSVYGWTQNPLI 116
                                                                                                                                                                                                                                                                                                                                                                                                                    43 IVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 QVQYTNLEGSRYQVRWRNJGNFVGGKGWNPGTG-RTINY-GCYFNPQGNGYLAVYGWTRN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 PLIEYYVVDSWGTYRP--TGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYYVVDSWGTYRP--TGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSK 163
A;Introns: 89/3
C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans A;Description:
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-9/Domain: signal sequence #status predicted <SIG>F;1-9/Domain: endo-1,4-beta-xylanase 1 #status predicted <MAT>F;44-221/Domain: endo-1,4-beta-xylanase homology <XYL>F;1-17,208/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                                                 9 LVGLSAALMSISLFSATASAASTDY-------WQN----WQN----WTDGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 RPTGSNATITFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 221;
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47.1%; Score 552; DB 2; Length 227;
Best Local Similarity 49.1%; Pred. No. 3.2e-34;
Matches 114; Conservative 28; Mismatches 54; Indels
                                                                                                                                                                                                                            41; Indels
                                                                                                                                                                                          49.3%; Score 577; DB 1; 50.7%; Pred. No. 4.2e-36; tive 38; Mismatches 41;
                                                                                                                                                                                                                                                             9 LVGLSAALMSISLFSATASAASTD---
                                                                                                                                                                                                                             Matches 116; Conservative
                                                                                                                                                                                                          Similarity
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Best Local (
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NiAlternate names: xylanase A
CiSpecies: Chaetcomium gracile
CjDate: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
CjAccession: 871472; 878206
RiYoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
Curr. Genet. 29, 73-80, 1995
A;Title: Two family G xylanase genes from Chaetcomium gracile and their expression in Asp
A;Reference number: 871472; MUID:96118924; PMID:8595661
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A;Residues: 31-45;82-94;152-160 <YOH>
A;Cross-references: UNIPARC:UP10000175A79; UNIPARC:UP10000175A82; UNIPARC:UP10000175A83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
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QSKRPTGSNATITFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTV 212
                                                                              <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Pathway: xylan degradation
C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase ho
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-30/Domain: signal sequence #status predicted <SIG>
F;1-21/9/Product: endo-1,4-beta-xylanase A #status experimental
F;42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
F;11-210/Domain: endo-1,4-beta-xylanase homology oxides of the control of the 
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49.1%; Pred. No. 2.4e-33;
tive 37; Mismatches 56; Indels
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Adv 9802

ADC27530 ADH10230 ADH10231 ADH10231 AAW60730 AAW60730 AAX18435 AAM60279 AAM60279 AAM60279 AAM60279 AAM60279 AAM60279 AAM18524 AAM18523 AAO18630 AAM18528 AAO18630 AAM18623 AAM18630 AAM18630 AAM18630 AAM18630 AAM18630 AAM18630 AAM18630 AAM18630 AAM18630 AAM18630

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AAY93752 standard; protein; 213 AA
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                                                                                                                                                                                                                                RESULT 1
Ady3752 A bacteri
Adc5599 Bacillus
Ad5599 Bacillus
Ad48518 Bacillus
Aab48518 Bacillus
Aab48518 Bacillus
Aab48518 Bacillus
Ad55008 Xylanase
Adi66728 B. subtil
Aay93755 A bacteri
Aay93754 A bacteri
Aay93751 A bacteri
Aay35086 Xylanase
Adj35086 Xylanase
Adj35086 Xylanase
Aay60732 Xylanase
Aay6073 Bacillus
Aau07391 Bacillus
                                                          ; Search time 199 Seconds
(without alignments)
470.290 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            US-10-626-724-5
1171
1 MFKFKKNFLVGLSAALMSIS......YQVMATEGYQSSGSSNVTVW 213
                                                                                                                                                                                                                                                                                                                                                                                                                      Description
        version 5.1.7
- 2006 Biocceleration Ltd.
                                                                                                                                                                            2443163
                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                          2443163 segs, 439378781 residues
                                                           February 3, 2006, 09:04:18
                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          - protein search, using sw model
                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                   A Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp290s:*
3: geneseqp2000s:*
4: geneseqp2002s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2004s:*
        GenCore
Copyright (c) 1993
                                                                                                                                                                                            seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                             Query
                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                           Run on:
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ALIGNMENTS

	×		
	E X	03-OCT-2000 (f	(first entry)
	DE X	A bacterial end	endo-beta-1,4-xylanase protein.
	₹ <u>₹</u>	Endo-beta-1,4-x	Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery produc
	₹ X	dough; dough preparation	eparation.
	88	Bacillus subtilis.	is.
	{ Z	WO200039289-A2.	
	X Q I	06-JUL-2000.	
	X E	17-DEC-1999;	99WO-IB002071.
	X 8	23-DEC-1998;	98GB-00028599.
	PR	06-APR-1999;	99GB-00007805.
	* *	16661-NAN-CT	- C1-00000-10-00
	<b>E</b>	(DANI-) DANISCO AS	AS.
	×:		
	Z X	Sibbesen O, So	Sorensen ur;
	DR	WPI; 2000-465744/40.	14/40.
	DR	N-PSDB; AAA47154.	.4.
	×	,	
	PT	Mutant xylanase	Mutant xylanase protein identified using xylanase inhibitor useful for
	PT	preparing non-e	preparing non-sticky dough for bakery products.
	PS	Claim 10; Page	Claim 10; Page 108; 112pp; English.
	X		
	႘	The present sec	The present sequence represents an endo-beta-1,4-xylanase. The
	ខ្ល	specification a	specification also describes an endo-beta-1,4-xylanase inhibitor, which
	ខ្ល	18 obtained fro	18 obtained from wheat flour. The specification also describes a mindal
-	88	xylanase protei	xylanase protein. The Xylanase is userul for preparing a looustuit,
	36	prererably a ba	preferably a bakery product of a substance (e.g. a dough) for making the product wild two evolanase or mutant xvlanase is useful for
	ខ	preparing a dou	on that is less sticky than a dough comprising a funga-
	ខ	xylanase. The x	xylanase. The xylanase inhibitor is useful for screening high degree
	ខ្ល	resistance xyla	resistance xylanases for dough preparation. The xylanase is also usefu
	ည _	tor preparing a	tor preparing a non-scicky dougn. A combination of xylamase and the

AAB48518 AAO18638 AAO18624 ADJ5008 ADI66728 ADI66728 AAY93755 AAY93754 AAY93754

AAY93751 ADO70164 ADJ35014 ADJ35086

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Matches

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ADO55909 standard; protein; 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 213, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fermentation; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-455433/43.
N-PSDB; ADO55908.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yoon HJ;
                                                                                                                                                                                                                                                                                                                  Sequence 213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KR2003015943-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO55909
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                                                                                                                                                                                                                                                                                 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
                                                                                                                                                                                                                                                                                                                  121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel variant xylanase protein or its fragment having xylanase activity. the variants have one or more amino acid modifications so that the protein or fragment has an altered sensitivity to a xylanase inhibitor and has an altered thermosensitivity as compared with a parent xylanase enzyme. The variant xylanases of the invention are useful for degrading or modifying a plant cell wall, and
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                                                                                                                                                                                                                                       61 TGNFVVGKGWTTGSPPRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                                                 1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                                                                                                                                                                      1 MFKFKKOPLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                                                                                                                                                                                                                  TGNFVVGKGWTTGSPPRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xylanase; xylanase inhibitor; thermosensitivity; plant cell wall; plant material; baking; processing cereal; starch production; processing wood; wood pulp bleaching; animal feed; flour separation; wetmilling; paper and pulp production; flour dough; hemicellulose; arabinoxylan; food supplement; xylan; baking process; bread volume; crumb structure; crumb appearance; shelf-life; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel variant xylanase polypeptide having altered sensitivity to a xylanase inhibitor and altered thermosensitivity as compared with a parent xylanase enzyme, useful in baking, processing cereals, starch
 calibrating and/or determining the quantity
                                                                                                                  ö
                                                                                Length 213;
                                                                                                                  Indels
                                                                                  DB 3;
                                                                           100.0%; Score 11.7,
100.0%; Pred. No. 1.8e-91;
rive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                  213
                                                                                                                                                                                                                                                                                                                                                                   181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis wild-type xylanase enzyme.
                                                                                                                                                                                                                                                                                                                                                  WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC27541 standard; protein; 213 AA.
inhibitor is useful for calibrativ
inhibitor in a wheat flour sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 1, 63pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-2002; 2002WO-IB003797.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                  213; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-332934/31.
N-PSDB; ADC27538.
                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DANI-) DANISCO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis.
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                                                   Sequence 213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC27541;
                                                                                  Query Match
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RESULT 2

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crearing a plant material. They may be useful for baking, processing acreals, starch production, in processing wood, and enhancing creb blacaching of wood pulp. They may also be useful for a variety of applications such as animal feed, flour separation (wetmilling) and paper and pulp production. In addition, they may also be useful for preparing a continuous such as animal feed, flour separation may alter or reduce the recosity derived from the presence of hemicallulose or arabinoxylan in a continuous sylamases in baking plant cell wall material, and for modifying colution or system comprising plant cell wall material, and for modifying continuous sylamases in baking processes improves the properties of flour based doughs and products made from the doughs. The baked products have highly desirable characteristics with respect to blood volume, crumb structure and additionally have an extended shelf-life. The enzymes of the invention have reduced thermosensitivity and inhibitor sensitivity, which allows a reduction in the amount of xylanase required for animal feed, starch production and baking. The present sequence is that of the full-length wild-type Bacillus subsilis xylanase which was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
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domestic animal; sawdust; pLYH7-39; bglC; xylanase; pLYH8-49; xynA;
pLYH8-62; xynD; pectate lyase; pLYH9-24; pelA; pLYH9-46; pelB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1171; DB 7; Length 213;
Pred. No. 1.8e-91;
; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis xynA protein sequence SeqID4.
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RESULT 5
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                                                                          This invention relates to novel genes encoding cellulase, cellulase expressed by the same, a microorganism containing the same gene, and an organic fertiliser using the same microorganism, therefore the organic fertiliser using the same microorganism, therefore the organic fertiliser can be rapidly produced from a mixture of the faeces and urine of domestic animals and sawdust. The microorganism Bacillus subtilis contains one cellulase encoding gene pLYH9-39 (pglC), two xylanase encoding genes pLYH9-49 (xynA) and pLYH9-46 (pelB) and two pectate lyase encoding genes pLYH9-24 (pelA) and pLYH9-46 (pelB). The organic fertiliser is produced by inoculating an appropriate amount of the microorganism and sawdust and fermenting the mixture. The present sequence is that of a Bacillus subtilis procein which is related to the production of the organic fertiliser of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; fungicide; thermostable xylanase activity;
dough conditioning; beverage production; nutritional supplement;
animal feed; lignin reduction; wood product; xylan; bacterial infection;
             microorganism
                                                                                                                                                                                                                                                                                                                              TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                                                                                                                                                                                                               1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                                                                                                                                                                                                                                                                                                                                                            TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                                                                                                                                                                                          Gaps
          Gene encoding cellulase, cellulase expressed by the same, micro
containing the same gene, and organic fertilizer using the same
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                   DB 7; Length 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylanase from an environmental sample seq id 188.
                                                                                                                                                                                                                                                                 100.0%; Score 1171; DB 7;
100.0%; Pred. No. 1.8e-91;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ34972 standard; protein; 213 AA
                                                        Claim 2; SEQ ID NO 4; 1pp; Korean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungal infection; coccidiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUN-2003; 2003WO-US019153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DIVE-) DIVERSA CORP.
                                                                                                                                                                                                                                             Sequence 213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steer B, Calle
Esteghlalian A;
                                    microorganism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-2004
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having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning; beverage production; as a mutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polymucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplification of a template nucleic acid with a primer pair capable of amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis. This is the amino acid sequence of a xylanase protein isolated from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                     useful for improving textile
                                                                                                                                                                                                                                                                            The invention describes an isolated or recombinant polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1171; DB 8; Length 213; 100.0%; Pred. No. 1.8e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                     Novel xylanase recombinant polypeptide useful for im
texture, treating paper, eliminating microorganisms.
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                                                                                                                                                                                                          Claim 60; SEQ ID NO 188; 570pp; English.
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2004-099016/10.
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                                       N-PSDB; ADJ34971
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Length 213; Indels 9 9 120

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TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is given in a specification relating to non maturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xylanase activity, enzyme; thermostable; xylanase; pulp bleaching; liquid clarification; coffee extraction; plant oil extraction; starch extraction; food thickener; animal food additive; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase, where protein has been modified to exhibit enhanced thermophilicity, alkalophilicity, or thermostability relative to naturally occurring B.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
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                                                                                                                                                                                                                                     99.7%; Score 1168; DB 3; 99.5%; Pred. No. 3.3e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                                       Local Similarity
nes 212; Conserv
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                                                                                                                                                                                             Sequence 213 AA;
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                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
                                                                                                                                                                                        The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
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                                                                                   alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
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                                                                 Non naturally occurring XA protein with enhanced thermophilicity,
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 1168; DB 3; Length 2 Pred. No. 3.3e-91; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus circulans endo-1,4-beta xylanase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                    Disclosure; Fig 16A; 114pp; English.
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                  WPI; 2000-679800/66
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 212; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 213 AA;
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circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bioconversion of lignocallulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase, where the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein, useful in bleaching process of pulp and industry, has enhanced thermostability and
                                                                                                                                                                                                                                                                                                                                                                                      TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endo-1,4-beta xylanase precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1A; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel xylanase activity
in food and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-608200/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alkalophilicity.
                                                                                                                                                                                            Sequence 213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-2002
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Matches
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protein has been modified to exhibit enhanced thermophilicity, alkalophilicity, or thermostability relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bloconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial; fungicide; thermostable xylanase activity;
dough conditioning; beverage production; nutritional supplement;
animal feed; lignin reduction; wood product; xylan; bacterial infection;
                                                                                                                                                                                                                                                                                                                           MFKFKKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                                                                                                                                                                                                                                                                                                                                                                                        61 TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                                                                                                                                                                                                        1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                                                                                                                                                                                                                                                                                                                                                                         TGNFVVGKGWTTGSPPRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
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                                                                                                                                                                                                                                         Score 1168; DB 5; Length 213;
Pred. No. 3.3e-91;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylanase from an environmental sample seg id 224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ35008 standard; protein; 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Callen W, Healey S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fungal infection; coccidiosis.
                                                                                                                                                                                                                                           99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-2003; 2003WO-US019153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2002; 2002US-0389299P
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                                                                                                                                                                                                                                                                          Matches 212; Conservative
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                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                              Sequence 213 AA;
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                                                                                                                                                                                                                                            Query Match
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The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable sylanase activity. (I) is useful for: dough conditioning; beverage production; as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis.
                                                                                                                                                                                                                                                                                                                                                                  environmental sample
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Sequence 213 AA;

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                                                                                                                         TGNEVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
                                                                                                                                                      61 TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
                                                                                                                                                                                    TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
                                                                                                                                                                                                    1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                              Gaps
                              ö
99.7%; Score 1168; DB 8; Length 213; 99.5%; Pred. No. 3.3e-91; ive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVW 213
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                               Conservative
           Local Similarity
hes 212; Conserv
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Query Match
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circulans endo-1,4-beta xylanase. ADI66728 standard; protein; 213 AA (first entry) 22-APR-2004 ADI 66728; 

Endo-1,4-beta xylanase, XA, EC 3.2.1.8; enzyme; bleaching; bleaching pulp; paper industry; food; animal feed; thermostability; alkalinophilic; hot alkali treatment.

Bacillus circulans

29. .213 /note= "Mature Xylanase" 1. .28 /note= "Signal peptide" Location/Qualifiers Peptide Protein

US6682923-B1

27-JAN-2004

99US-0133714P. 12-MAY-2000; 2000US-00570856 12-MAY-1999; 07-JUN-1999;

(XENC-) XENCOR

99US-0133714P. 99US-0138156P.

12-MAY-1999; 07-JUN-1999;

Dahiyat BI; Bentzien J,

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The invention relates to a mutant xylanase activity (XA, endo-1,4-beta xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a bleaching agent comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADI66728. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 59, 105, 144. The non-naturally occurring xylanase activity (XA) protein is useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence represents the wild-type xylanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                                                                            New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.7%; Score 1168; DB 8; Length 213; 99.5%; Pred. No. 3.3e-91; ive 1; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.5
Matches 212; Conservative
                 WPI; 2004-118575/12.
N-PSDB; ADI66729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 213 AA;
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Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp; paper industry; food; animal feed; thermostability; alkalinophilic; hot alkali treatment. ADI66740 standard; protein; 213 12-MAY-2000; 2000US-00570856. (first entry) B. subtilis xylanase. Bacillus subtilis. US6682923-B1. 22-APR-2004 27-JAN-2004 AD166740; RESULT 11 

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The present sequence represents a mutant endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product, wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree for preparing a non-sticky dough. A combination of xylanase is also useful inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endo-beta-1, 4-xylanase inhibitor; wheat flour; xylanase; bakery product;
                                                                                                                                                                                                                                    Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGTVNAVNGSGGNYSVNWSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IGNFVVGKGWITGSPFRIININAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.1%; Score 1161; DB 3; Length 213; 99.1%; Pred. No. 1.3e-90; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "wild type Ile changed to Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                     Claim 1; Page 111; 112pp; English.
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98GB-00028599.
99GB-00007805.
99GB-00008645.
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                                                                                                                               JF;
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Matches 211; Conservative
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                                                                                                                               Sorensen
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                                                                                       (DANI-) DANISCO AS.
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Bacillus subtilis.
                                                                                                                                                                                                N-PSDB; AAA47157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 213 AA;
  23-DEC-1998;
06-APR-1999;
                                               15-APR-1999;
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                                                                                                                                                                                                                                                      The invention relates to a mutant xylanase activity (XA, endo-1,4-beta xylanase from Bacillus circulans) protein appearing as AD166730. Also included is a bleaching agent comprising the XA protein. The non-naturally occurring XA protein comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase AD166728. The anino acid substitutions are made at positions 26, 38, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 51, 58, or 144. The non-naturally occurring xylanase activity (XA) protein is also useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring yylanases, simplifying incorporation of the xylanase treatment step into pulp processingly especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species included for comparison.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MFKFKKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIBYYVVDSWGTYRPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
                                                                                                                               New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1168; DB 8; Length 213;
Pred. No. 3.3e-91;
1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WKSHGMNLGSNWAYQVMATEGYOSSGSSNVTVW 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacterial endo-beta-1,4-xylanase mutant XM3.
                                                                                                                                                                                                                     Disclosure; SEQ ID NO 13; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY93755 standard; protein; 213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-IB002071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.5
Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dough; dough preparation.
                                               Dahiyat BI;
                                                                                       WPI; 2004-118575/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 213 AA;
    (XENC-) XENCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200039289-A2
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                                               Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-2000
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RESULT 15
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ID AAR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNAAITFSNHVNA 180
                                                                                                                                                                                                                                                                                     The present sequence represents a mutant endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree for preparing a non-sticky dough. A combination of xylanase and the inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample
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dough; dough preparation.
                                                                                                                                                                                                                               Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGTVNAVNGSGGNYSVNWSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
         /note= "wild type Gln changed to Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.5%; Score 1154; DB 3;
98.1%; Pred. No. 5.1e-90;
ive 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A bacterial endo-beta-1,4-xylanase mutant XM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93754 standard; protein; 213 AA
                                                                                                                                                                                                                                                                  Claim 1; Page 109; 112pp; English
                                                                              99WO-IB002071
                                                                                                    98GB-00028599
                                                                                                                99GB-00007805
99GB-00008645
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                                                                                                                                                                         Sorensen JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.1
Matches 209; Conservative
                                                                                                                                                                                               2000-465744/40.
203
                                                                                                                                                  (DANI-) DANISCO AS.
                                                                                                                                                                                                          N-PSDB; AAA47155
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 213 AA;
Misc-difference
                                WO200039289-A2
                                                                              17-DEC-1999;
                                                                                                                                                                        Sibbesen O,
                                                                                                    23-DEC-1998;
                                                                                                                           15-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification also describes an endo-beta-1.4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparating a non-sticky dough. A combination of xylanase and the inhibitor is useful for callibraring and/or determining the quantity of inhibitor in a wheat flour sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a mutant endo-beta-1,4-xylanase. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.1%; Score 1149; DB 3; 97.7%; Pred. No. 1.3e-89; tive 2; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 110; 112pp; English
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                                                                                                                                                                                                                             98GB-00028599.
99GB-00007805.
99GB-00008645.
                                                                                                                                                                     99WO-IB002071.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Sibbesen O, Sorensen JF;
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Matches 208; Conservative
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N-PSDB; AAA47156.
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Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 213 AA;
                                                           WO200039289-A2
                                                                                                                                                                           17-DEC-1999;
                                                                                                                                                                                                                                   23-DEC-1998;
06-APR-1999;
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10-AUG-1994
                                                                                                                   06-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MFKFKKKFLVGLTAAFWSISMFSATASAAGTDYWQNWTDGGGTVNAVNGSGGNYSVNWSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The modified xylanase is used as a baking agent, preferably for yeast pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Xylanase; Bacillus subtilis; baking; bread; yeast; food; foodstuffs;
bread; pastry.
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type amino acid substituted for Lys."
                                                                                                                                                                                                  note= "Wild type amino acid substituted for Phe."
                                                                                                                                                                                                                               note= "Wild type amino acid substituted for Met."
                                                                                                                                           'note= "Wild type amino acid substituted for Lys."
                                                                                                                                                                      note= "Wild type amino acid substituted for Thr."
                                                                                                                                                                                                                                                                                      note= "Wild type amino acid substituted for Gly."
                                                                                                                                                                                                                                                                                                                   note= "Wild type amino acid substituted for Thr."
                                                                                                                                                                                                                                                                                                                                              note= "Wild type amino acid substituted for Asn."
                                                                                                                                                                                                                                                                                                                                                                            note= "Wild type amino acid substituted for Ala."
                                                                                                                                                                                                                                                                                                                                                                                                        note= "Wild type amino acid substituted for Leu."
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96.5%; Score 1130; DB 2; Length 213;
Best Local Similarity 95.3%; Pred. No. 5.6e-88;
Matches 203; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                    1. .28
/label= Signal peptide.
                                                                                                                                                                                                                                              29. .185
/label= Mature protein.
                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gottschalk M, Sproessler B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92DE-04226528.
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N-PSDB; AAQ56052.
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181 WKSHGMNLGSNWAYQVLATEGYKSSGSSNVTVW 213 셤

Search completed: February 3, 2006, 09:08:08 Job time : 201 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

February 3, 2006, 09:04:53 ; Search time 246 Seconds (without alignments) 610.884 Million cell updates/sec Run on:

US-10-626-724-5 1171 1 MFKFKKNFLVGLSAALMSIS......YQVMATEGYQSSGSSNVTVW 213

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	P18429 bacillus su				bacillus		10	Q84f19 bacillus sp	Q8vvc3 bacillus sp		Q6tlp3 uncultured	P45705 bacillus st			Q9kef3 bacillus ha		Q9rqb8 xylanimicro			•		Q9rmm4 streptomyce	Q76bv2 streptomyce			Q9ew89 streptomyce				392	P54865 cellulomona
CI.	XYNA BACSU	XYNA_BACCI	Q59254_BACSU	Q59256_9BACI	Q8RMN9_BACSU	Q8RMN8 BACCI	Q9ZB36_BACSP	Q84F19 9BACI	Q8VVC3_9BACI	Q9F9B9_9BACL	Q6TLP3 9BACT	XYNA BACST	Q43993_AERPU	Q71S35_BACFI	Q9KEF3_BACHD	Q6U894_BACFI	Q9RQB8_9MICO	Q56265_THEFU	QSRZ98_THEFU	Q9RI72_STRCO	Q9RMH9_STRVD	Q9RMM4_STRTM	Q76BV2_STRTL	XYNC STRLI		Q9EW89_STROI	Q59962_9ACTO	Q4WG11_ASPFU	Q56013_9ACTO	Q693B5_9ALTE	XYND_CELFI
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Q8VUT4 9PSED XYNA EMENI	OSB767 EMENI XYNB STRLI	Q9RKN6_STRCO Q7SDQ1_NEUCR Q8J1V5_9PEZ1	Q8TG22_ASPNG Q6QA21_9EURO	OSAQRS EMENI XYNZ ASPNG O9HFA4 ASPOR	XYNB_BMENI XYNB_ASPKA
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## ALIGNMENTS

RESULT XYNA B ID X AC D DT 00	LT 1  BACSU STANDARD; P18429; 01-NOV-1990 (Rel. 16, Creat
8888	<pre>10-MAX-2005 (Rel. 4'), Labt annotation update) Endo-1,4-beta-xylanae A precursor (EC 3.2.1.8) (Xylanase A) (1,4- beta-D-xylan xylanohydrolase A). Name=xynA; OrderedLocusNames=BSU18840;</pre>
888	Bacillus subtilis. Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCHT TOSTHO-1403.
2	NOT TAXIDELYS); NUCLEOTIDE SEQUENCE.
RT RA	Paice M.G., Bourbonnais R., Desrochers M., Jurasek L., Yaguchi M.; "A xylanase gene from Bacillus subtilis: nucleotide sequence and
RT RL	comparison with B. pumilus gene."; Arch. Microbiol. 144:201-206(1986).
R.P.	[2] NUCLEOTIDE SEQUENCE.
Z Z	Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.; "Sequence analysis of the Bacillus subtilis chromosome region between
RT	the terc and odhAB loci cloned in a yeast artificial chromosome.";
Z Z	
8 P	NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA). STRAIN=168:
XX a	MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786; Kningt F. Organwara N. Moszer I. Albertini A.M. Alloni G.
<b>2</b>	Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA S	A Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
<b>5</b> 2 1	Choi SK., Codani JJ., Connerton I.F., Cummings N.J., Daniel R.A.,
<b>8</b> 8	Denizot F., Devine K.M., Duesternoeit A., Enriich S.D., Emmerson F.I., Entian KD., Errington J., Pabret C., Ferrari E., Foulger D.,
88	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Chim S., Glasor D. Coffean B. Colichtly R.J. Grandi G.
<b>5 2</b> 1	Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
<b>8</b> 8	Hilbert H., Holsappel S., Hosono S., Hullo MF., Itaya M., Jones LM., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
2:	Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
<b>S</b> S	Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee SM., Levine A., Liu H., Masuda S., Mauel C.,
25	Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
¥ 6	Noback M., Noone D., O'Kellly M., Ogawa K., Ogiwara A., Oudega B., Park SH. Parro V. Pohl T.M. Portetelle D., Porwollik S.,
[2:	Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
8 8 8	Rey M., Reynolds S., Rleger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
æ	Serror P.,
8 8	Shin BS., Soldo B., Sorokin A., Tacconi E., Takagı T., Takanashı H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
R.	Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,

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                                                                                                                                                                                                                                                                         Wakarchuk W., Methot N., Lanthier P., Sung W., Seligy V., Yaguchi M.,
To R., Campbell R., Rose D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M36648; AAA22897.1; -; Genomic_DNA.

EMBL; AF027868; AAA8458.1; -; Genomic_DNA.

EMBL; A29114; CAB13776.1; -; Genomic_DNA.

EMBL; 299114; CAB13776.1; -; Genomic_DNA.

EMBL; 299114; CAB13776.1; -; Genomic_DNA.

PDB; 1AXX; X-ray; A/B=-.

R PMS; P18429; 27-213.

R Subtilist; BG10808; xynA.

R InterPro; IPR001137; Glyco_hydro_11.

PRM; PR00457; Glyco_hydro_11; 1.

PRNTS; PR00911; GLHYDRLASE11.

R PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.

BD-structure; Complete profeome; Glycosidase; Hydrolase; Signal; A Xylan degradation.
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(In) Visser J., Beldman G., Kusters-van Someren M.A., Voragen A.G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                        L7.1VE SITE GLU-106.
MEDLINE=94271752; PubMed=7911679;
Miao S., Ziser L., Aebersold R., Withers S.G.;
"Identification of glutamic acid 78 as the active site nucleophile :
Bacillus subtilis xylanase using electrospray tandem mass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gpectrometry.";
Biochemistry 33:7027-7032(1994).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
linksges in xylans.
-!- PATHWAY: Xylan degradation.
-!- SAMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase).
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                                                                                                                                                                                                                                                                                                                                                                                        Xylans and xylanases, pp.439-442, Elsevier, Amsterdam (1992)
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ive 0; Mismatches 0;
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                                                                                                                                                                                         Nature 390:249-256(1997).
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Matches 213; Conservative
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                                                                                                                                                                                                    (Xylanase) (1,4-beta-D-
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R PDB; 1C5I; X-ray; A=29-213.

R PDB; 1HV1; X-ray; A=29-213.

R PDB; 1HV1; X-ray; A=29-213.

R PDB; 1HV1; X-ray; 0=29-213.

R PDB; 1XNB; X-ray; 0=29-213.

R PDB; 1XNC; X-ray; 0=29-213.

R PDB; 1XNC; X-ray; 0=29-213.

R PDB; 2BVV; X-ray; A=29-213.

R PDB; 2BVV; X-ray; A=29-213.

R PDB; 2BVV; X-ray; A=29-213.

R PROSTE; PSO0776; GLYCOSYL HYDROL_F11; 1.

R PROSTE; PSO0776; GLYCOSYL HYDROL_F11; 1.

R PROSTE; PSO0777; GLYCOSYL HYDROL_F11; 1.

R PROSTE; PSO0776; GLYCOSYL HYDROL_F11; 1.

R PROSTE; PSO0777; GLYCOSYL HYDROL_F11; 1.
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MEDLINE-56122131; PubMed=8756457; DOI=10.1021/bi9613234;

MCINTOSH L.P., Hand L., Johnson P.E., Joshi M.D., Koerner M., Plesniak L.A., Ziser L., Wakarchuk W.W., Withers S.G.; I'the pka of the general acid/base carboxyl group of a glycosidase cycles during catalysis: a 13C-NMR study of Bacillus circulans
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-!- PATHWAY: Xylan degradation.
-!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 35:9958-9966(1996).
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Yang K.C.A., MacKenzid C.R., Narang S.A.;
"Nucleotide sequence of a Bacillus circulans xylanase gene.";
Nucleic Acids Res. 16:7187-7187(1988).
                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1397;
                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS), AND MUTAGENESIS
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Nucleophile.
Proton donor.
01-WAR-1989 (Rel. 10, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Endo-1,4-beta-xylanase precursor (EC 3.2.1.8)
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NUCLEOTIDE SEQUENCE
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STRAIN=168 trpC2
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MEDLINE=55219081; PubMed=7704256;
MEDLINES=52219081; PubMed=7704256;
Wolf M., Geczi A., Simon O., Borriss R.;
"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenses. cellulase and xylanase.";
Microbiology 141:281-290(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN
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                                                                                                                                                                                                                                                                                                                                                     Score 1168; DB 1; Length 213;
Pred. No. 4e-86;
1; Mismatches 0; Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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Last annotation update)
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MEDLINE=92140374; PubMed=1310524;
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illarity 99.5%;
Conservative
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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Q59254 BACSU PRELIMINARY;
Q59254;
 Xylanase (EC 3.2.1.8)
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NUCLEOTIDE SEQUENCE.
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213 AA;
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NUCLEOTIDE SEQUENCE
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Matches 212; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 213;
Borriss R., Wolf M.;
Submitted (UUL-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (UUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z34519; CAA84276.1; -; Genomic_DNA.
HSSP; 090850; IXNB.
SNR; 059264; 27-213.
GO; GO:001176; F:endo-1,4-beta-xylanase activity; IEA.
GO; GO:0065493; P:xylan catabolism; IEA.
Interpro; IPRO01137; Glyco-hydro-11.
Pfam; PF00457; Glyco-hydro-11.
PRINTS; PR00911; GLHYDRLASE11.
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Submitted (DEC-1990) to the EMBL/GenBank/DDBJ databases.
EMBL; X59058; CA441783.1; -; Genomic_DNA.
FTR; 548126; S48126.
HSSP; P09850; LWB.
SNR; Q95256; 27-213.
GO; GO:001176; F:endo-1,4-beta-xylanase activity; IEA.
GO; GO:001175; F:endo-1,4-beta-xylanase activity; IEA.
CO; GO:001175; F:endo-1,4-beta-xylanase activity; IEA.
CO; GO:001137; Glyco-hydrolism; IEA.
InterPro; IPR001137; Glyco-hydroll.
PEAm; PF004591; GLYCo-hydroll.
PEAm; PF004591; GLYCo-hydroll.
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Bacillus sp. YA-14.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxIb=72411;
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PROSITE; PS00777; GLYCOSYL HYDROL F11_2; 1.
Glycosidase; Hydrolase; Xylan degradation.
SEQUENCE 213 AA; 23355 MW; 21D76D4FEBCED4B7 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Endo-1, 4-beta-xylanase precursor (EC 3.2.1.8).
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99.5%; Pred. No. 5.8e-86;
iive 0; Mismatches 1;
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Q59256;
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Matches 212; Conservative
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QBRMNB_BACCI PRELIMINARY;
QBRMNB;
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Q9ZB36;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                        DB 2; Length 213;
                                                                                                                                                                                                0; Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, FA490979; AAM08359.1; -; Genomic_DNA.
HSSP; P09856.1 IXNB.
SMR; QBRNN9; 27-213.
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                                                                                  29 213 endo-1, 4-beta-xylanase.
213 AA; 23341 MW; 2110D35768CC0034 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1. BROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1. BLYCOSYL_HYDROL_F11_2; 1. 28 CAGNAL; XVlan_degradation. SIGNAL
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                                                                                                                                                      Query Match
99.5%; Score 1165; DB 2
Best Local Similarity 99.1%; Pred. No. 7e-86;
Matches 211; Conservative 2; Mismatches
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QBRMN9;
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Matches 210; Conservative
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121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF490980; AAM08360.1; -; Genomic_DNA.
HSSP; P09560; IXMB.
SMR; Q8RMN8; 27-213.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl .
GO; GO:00045975; P:xylan catabolism; IEA.
GO; GO:00045975; Garbohydrate metabolism; IEA.
InterPro; IPR001137; Glyco_hydro_ll.
PRINTS; PR00911; GlyTROLAFELI.
PROMITS; R000911; GLYCOSYL_HYDROL_FIL.1; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Endo-1,4-xylanase.
Bacillus circulans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Kim S.C., Jeong K.J., Kim M.S.;

Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; 191675; AAD10834.1; -; Genomic_DNA.

HSSP; P09856; 1XNB.

SWR; Q9ZB36; 27-213.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Endo-1,4-beta-xylanhydrolase.
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181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVW 213
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61 TGNFVVGKGWITGSPFRINYNAGVMAPNGNAYLILYGWIRSPLIEYYVVDSWGTYRPIG
1 MFKFTKKFLVGLTAALMSISLFSANASAANTDYWQNWTDGGGTVNAVNGSGGNYSVNWSN
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(TrEMBLrel. 16, I
(TrEMBLrel. 26, I
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09F9B9 9BACL PRELIMINARY;

09F9B9;

01-MAR-2001 (TrEMBLrel. 16,

01-MAR-2004 (TrEMBLrel. 16,
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Q8VVC3;
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Matches 197; Conservative
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GO; 0004553; P:hydrolase activity, hydrolyzing O-glycosyl
GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl
GO; GO:004553; P:xylan catabolism; IEA.
InterPro; IPR001137; Glyco_hydro_11.
PERN; PR0091; GLYCOSYL_HYDRO_11; 1.
PROSITE; PR0091; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Signal; Xylan degradation.
Potential.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl
GO; GO:000975; P:carbohydrate metabolism; IEA.
InterPro; IPR00113; Glyco_hydro_11.
Pram; PR00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRLASE11.
PROSTIE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
                                                                                                                                                                                                                            ttch 96.2%; Score 1127; DB 2; Length 213; sal Similarity 94.8%; Pred. No. 8e-83; 202; Conservative 5; Mismatches 6; Indels (
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=126733;
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                                                                                                                                                                                      213 AA; 23277 MW; 3AIDEE1139E3358B CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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Name=xynA;
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Q84F19;
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SEQUENCE
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Best Local
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121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
                           TGNEVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=165829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hong I.P., Lee S.Y., Choi S.G.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF441773; AAL32473.1; -; Genomic_DNA. HSSP; P09856; IXNB. SMR; Q8VVC3; 27-213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 AA; 23341 MW; 4CC0DFFF525E7551 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                        181 WKRYGMNLGSNWSYQVLATEGYQSSGSSNVTVW 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
                                                                                                          WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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SEQUENCE REVISION.
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P45705;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 SGNFVVGKGWTTGSPDRTINYNAGVWAPSGNGYLALYGWTRNSLIEYYVVDSWGTYRPTG 119
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Xylanase A.
Paenibacillus sp. KCTC8848P.
Bacteria; Firmicutes; Bacillales; Paenibacillus.
NCBL_TaxID=109199;
                                                                                                                                                                                                                                                                               Lee H.J., Shin D.J., Cho N.C., Im S.Y., Lee H.B., Chun S.B., Bai Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL, AF195421; AG23526.1; -; Genomic_DNA.

R HSSP, P09850; IXNB.

R GO; GO:0004593; E:hydrolase activity, hydrolyzing O-glycosyl . GO; GO:0004593; P:hydrolase activity, hydrolyzing O-glycosyl . GO; GO:0004593; P:hydrolase activity, hydrolyzing O-glycosyl . GO; GO:0004593; P:hydrolase activity, hydrolyzing O-glycosyl . R GO; GO:0004593; P:hydrolase activity, hydrolyzing PRO0137; Glyco-hydrolase, IRA.

R PRONIE; PRO0137; Glyco-hydrolase, IRA.

R PRINTS; PRO0991; GLYCOSYL_HYDROL_FIL 1; UNKNOWN_I.

R PROSITE; PS00776; GLYCOSYL_HYDROL_FIL 2; I.
                                                                                                                                                                                                                                                                                                     Chun S.B., Bai
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PubMed=14718652; DOI=10.1110/ps.0333504;

Palackal N., Brennan Y., Callen W.N., Dupree P., Frey G., (A Palackal N., Brennan Y., Callen W.N., Dupree P., Frey G., (A Palacwood G.P., Healey S., Kang Y.E., Kretz K.A., Lee E., Tomlinson G.L., Verruto J., Wong V.W.K., Mathur E.J., Shori Proberison D.E., Steefe B., Frey G., (A Roberison D.E., Steefe B., Frey G., (B Protein Sci. 13:494-503(2004).

Rembl., Ay394562, AAQ90180.2; -; Genomic_DNA.

RESP; PO9850; DECX.

SMR; QFILP3; 30-214.

RGO; GO:0005975; P:carbohydrate metabolism; IEA.

RGO; GO:0005975; P:carbohydrate metabolism; IEA.

RGO; GO:0005975; P:carbohydrate metabolism; IEA.

RFAN; PROM513; Glyco.hydro.ll.

RFAN; PROM513; Glyco.hydro.ll.

RFAN; PROM511; GLHYDRLASE11.
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80.7%; Score 945.5; DB 2; Length
Best Local Similarity 79.3%; Pred. No. 3.2e-68;
Matches 169; Conservative 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 AA; 23258 MW; 1A1ABC825BED93D2 CRC64;
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OGTLB3;
OG-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
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                                                                                                                                                                                                                                                            STRAIN=KCTC 8848P,
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OGTLP3 9BE
TO GGTLP3 9BE
TO GS-JJ
DT 05-JJ
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                       1 MFKLSKKILMVLLTISMSFISLFTVTAYAASTDYWQNWTDGGGTVNATNGSDGNYSVSWS
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                                                                                                                                                                                                                                                                                      1 MFKFKKNFLVGLSAALMS-ISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linkages in xylans.
-!- PATHWAY: Xylan degradation.
-!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cho S., Choi Y.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    Query Match 79.9%; Score 935.5; DB 2; Length 214; Best Local Similarity 80.4%; Pred. No. 2.1e-67; Matches 172; Conservative 13; Mismatches 28; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
                                                                                                                  6FD1CB9BB66A5048 CRC64;
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HSSP; P09850; IXNB.
SMR; P45705; 24-210.
Interpro; IPR001137; Glyco_hydro_11.
Pfam; PP00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRIASE11.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Glycosidase; Hydrolase; Signal; Kylan degradation.
SIGNAL
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Glycosidase; Hydrolase; Signal; Xylan degradation.
SIGNAL 1
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J. Microbiol. Biotechnol. 5:117-124(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
                                                                                                                  214 AA; 23478 MW;
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Bacillus stearothermophilus
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Best Local Similarity 74.2%
Matches 158; Conservative
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Q71S35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylan degradation.
SEQUENCE 210 AA;
                                                                                                                                                                                                                                                                                                                     Xylanase.
Bacillus firmus.
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                                                                                                                                                                                                                  KGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNAWK 182
                                                                                                                                                                                                                                KGTVNSDGGTYDIYTTMRYNAPSIDGTQ-TPQQFWSVRQSKRPTGSNVSITFSNHVNAMR 179
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                                                                                                                                                                                KLKKKMLTLLLTASMSFGLFGATSSAA-TDYWQYWTDGGGMVNAVNGPGGNYSVTWQNTG
                                                                                                                3 KFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=ME-1; TISSUE-Gut content of silk worm;
Suzuki T., Itoh Y., Naito H., Kubata K.B., Horitsu H., Takamizawa K.,
Kawai K.;
                                                                                        Gaps
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STRAIN=ME-1; TISSUE=Gut content of silk worm;
Kubata K.B., Suzuki T., Horitsu H., Kawai K., Takamizawa K.;
"Xylanase I of Aeromonas caviae ME-1 isolated from the intestine herbivorous insect(Samia cynthia pryeri).";
Biosci. Biotechnol. Biochem. 56:1463-1464(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aeromonas punctata (Aeromonas caviae).
Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
Aeromonadaceae; Aeromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OGN. GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl GO: GO:0005975; P:carbohydrate metabolism; IEA. GO: GO:0005975; P:carbohydrate metabolism; IEA. GO: GO:0005975; P:carbohydrate metabolism; IEA. InterPro; IPR001137; Glyco hydro_11. PRINTS; PR00911; GLYCOSYL HYDROL PROSITE; PS00776; GLYCOSYL HYDROL FIL 1; UNKNOWN_1. PROSITE; PS00777; GLYCOSYL HYDROL_FIL_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of the xynA gene encoding an endo-xylanae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.3%; Score 929; DB 2; Length 211; 79.3%; Pred. No. 6.8e-67;
                                                               Length 210;
210 Endo-1,4-beta-xylanase A.
104 Nucleophile (By similarity).
23221 MW; 3190CF74C34AAB45 CRC64;
                                                                                        28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1) of Aeromonas caviae ME-1.";
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, D32065; BAA06837.1; -; Genomic_DNA.
HSSP: P09869; IXNB.
SMR; Q43993; 25-211.
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                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                               79.4%; Score 930; DB 1;
80.6%; Pred. No. 5.6e-67;
                                                             Query Match 79.4%; Score 930; DB 1
Best Local Similarity 80.6%; Pred. No. 5.6e-6
Matches 170; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                     SHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                                                                                                                                                                                                                             211 AA
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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IGNAL 1 28
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Q43993;
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 20 2
104 1
197 1
210 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=xynA;
 CHAIN
ACT_SITE
ACT_SITE
SEQUENCE
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TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
                                                                                       60 TGNFVVGKGWTYGTPNRVVNYNAGVFAPSGNGYLTFYGWTRNALIEYYVVDSWGTYRPTG 119
                                                                                                                                       TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
                                                                                                                                                         TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIBYYVVDSWGTYRPTG 120
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                    1 MFKFGKKLMTVVLAASMSFGVFAATSSAA-TDYWQNWTDGGGTVNAVNGSGGNYSVSWQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=1399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 AA; 23313 MW; AC4BASDD5D67A1B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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OFKETS BACHD PRELIMINARY;
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Martinez M.A., Delgado O.D., Breccia J.D., Sineriz F.;
Submirted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
Submirted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BA000004; BAB04618.1; -; Genomic_DNA.
EMBL; AY170624; AA012276.1; -; Genomic_DNA.
EMBL; AY170624; F.Hydrolase activity; IEA.
GO; GO:0016787; F.Hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
GO; GO:0005975; P.carbohydrate metabolism; IEA.
InterPro; IPR001137; Glyco_hydro_ll: 1.
Pfam; PF00457; Glyco_hydro_ll: 1.
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                                                                                                                                                                                                                                                                                                                                                     MEDINE=22269261; PubMed=12382115; DOI=10.1007/s00792-002-0269-4; Martinez M.A., Delgado O.D., Breccia J.D., Baigori M.D., Sineriz F.; Revision of the taxonomic position of the xylanolytic Bacillus sp. MIR32 reidentified as Bacillus halodurans and plasmid-mediated Exransformation of B. halodurans."; Extremophiles 6:391-395(2002).
                                                                                                                                                                                                                                             "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.", Nucleic Acids Res. 28:4317-4331(2000).
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                                                                                                                                                           STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                   Endo-1,4-beta-xylanhydrolase.
Name-xynllA, OrderedLocusNames=BH0899;
Bacillus holdurans
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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PR051TE; PS00777; ĞLYCOSYL HYDROL_F11_2; 1.
COMPLETE PC1000me; HYDROLJASE.
SEQUENCE 210 AA; 23313 MW; AC4BASDDSD67A1B2 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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                                                                                                         NCBI_TaxID=86665;
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Search completed: February 3, 2006, 09:12:20 Job time : 249 secs

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5, Appl.
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1 MFKFKKNFLVGLSAALMSIS......YQVMATEGYQSSGSSNVTVW
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5.1.7
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
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US-08-104-445-3
US-08-044-621D-37
US-09-047-370-5
US-08-044-621D-36
US-09-912-3
US-09-970-856B-9
US-09-570-856B-7
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US-09-570-856B-1:
US-08-315-695-21
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 GenCore version (c) 1993 - 2006
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Gapop 10.0 , Gapext 0.5
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-770-621- -235-832- -315-695- -744-5708 -744-5708 -744-5210 -047-370- -570-8568 -709-912- -708-373- -708-273- -748-373- -748-373- -748-373- -748-373- -748-373- -748-373- -748-373- -748-373- -748-373- -748-373- -748-6210	ALIGNMENTS	LE ALK K 0,856B 714	1168; No. 6. smatche	ASAAST         ASAAST	WAPNGN        WAPNGN
US-09-770-621-2 US-09-235-832-2 US-08-315-655-20 US-07-744-570B-2 US-08-709-9121-3 US-08-709-9121-10 US-08-044-621D-34 US-08-047-370-11 US-08-044-621D-34 US-08-044-621D-34 US-08-047-370-10 US-08-047-370-10 US-08-047-370-10 US-08-044-621D-38 US-08-044-621D-38 US-08-044-621D-38 US-08-044-621D-38 US-08-044-621D-38 US-08-044-621D-38 US-08-044-621D-38	ALI	ULT 1 09-570-856B-1 dequence 1, Application US/09570856B atent No. 6682923 ENERAL INFORMATION: APPLICANT: Bentzien, Joerg M APPLICANT: Bentzien, Joerg M APPLICANT: Bentzien, Joerg M APPLICANT: Bentzien, Joerg M APPLICANT: Bentzien, Sorg M APPLICANT: Bentzien, Sorg M APPLICANT: Dahiyat, Bassil I TITLE OF INVENTION: NOVEL THERMOSTABLE. FILE REFERENCE: A 67474B-1/RFT/RMS/RM/ CURRENT FILING DATE: 2002-04-15 PRIOR APPLICATION NUMBER: US 60/133,714 PRIOR FILING DATE: 1999-05-12 NUMBER OF SEQ 1D NOS: 34 SOFTWARE: Patentin version 3.1 EAGUID NO 1 LENGTH: 213 TYPE: RET TYPE: RECORDING: SORGANISM: Bacillus circulans FRATURE: NAME/KEY: SIGNAL LOCATION: (1)(28) OTHER INFORMATION: FEATURE: NAME/KEY: mat_peptide LOCATION: (29)(3) OTHER INFORMATION: OTHER INFORMATION:	Score Pred. 1, Mia	SLFSAT        SLFSAT	NYNAGV         NYNAGV
00444444044004404		0957 I M THER THER THER 1. 13.1 1. 3.1	**	TWSI	FRTI 
3444 2144 2162 200 200 200 3315 191 191 183 183 183		ion US/0957 ion US/0957 i, Joerg M NOVEL THER 7478-1/RFT, 7478-1/RFT, 11 NUMBER: US 11999-05-12 83: 34 version 3.1 circulans icirculans ide	99 99 vativ	VGLSAP VGLSAP	WTTGSE        WTTGSE
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		ULT 1 09-570-856B-1 equence 1, Application US/095 atent 0. 668223 ENERAL INFORMATION: APPLICANT: Bentzien, Joerg M APPLICANT: Bentzien, Joerg M ATTILE OF INVENTION: NOVEL THI TITLE OF INVENTION: NOVEL THI FILE REFERENCE: A-67478-1/RF CURRENT APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-05-12 NUMBER OF SEQ ID NOS: 34 SOFTWARE: PREMENT: 133 TYPE: RT ORGANISM: Bacillus circulans FEATURE: NAME/KEY: SIGNAL LOCATION: (1)(28) OTHER INFORMATION: FEATURE: NAME/KEY: MAE_DEPLIGE NAME_MAE_DEPLIGE NAME_DEPLIES NAME_MAE_DEPLIES NAME_MAE_DE	Similarity 2; Conservat	FKKNFL        FKKNFL	PVVGKG         PVVGKG
		856B-1 io. 6682923 INFORMATION INT: Bentzie INT: INT: INT: INT: INT: INT: INT: INT:	Simi 2;		
636 636 637 618 618 618 618 618 618 636 636 636 636 636 636 636 636 636 63		ULT 1 09-570-856B-1 actant No. 6682923 ENERAL INFORMATION APPLICANT: Bentzier APPLICANT: Bentzier APPLICANT: Bentzier APPLICANT: Bentzier APPLICANTON CURRENT FILLE REFERENCE: A-(CURRENT FILLE DEPLICATION) PRIOR APPLICATION I PRIOR APPLICATION I PRIOR PELLONION I PRIOR PELLING DATE: CURRENT FILLING DATE: CURRENT FILLING DATE: CURRENT FILLING DATE: NUMBER OF SEQ ID NO. 1 LENGTH: 213 LENGTH: 213 LENGTH: 213 LENGTH: 213 LENGTH: 213 LOCATION: (1) (20) COCATION: (1) (20) COCATION: (2) (COCATION: (2) (C	Match local ss 21	<b>н</b> н	61
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FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN 60
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                                                     GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Bentzien, Joerg M
APPLICANT: Delniyat, Basail I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REPERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570, 856B
CURRENT FILING DATE: 2002-04-15
PRIOR PILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
IENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1168; DB 2; Length 213;
Pred. No. 6.3e-98;
1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Liungdahl, Lars G.
TITLE OF INVENTION: Aureobasidium Pullulans Xylanase, Gene
TITLE OF INVENTION: and Signal Sequence
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                Sequence 13, Application US/09570856B Patent No. 6682923
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Patent No. 5591619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.7%;
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.5'
Matches 212; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat_peptide;
LOCATION: (29)..()
CTHER INFORMATION:
US-09-570-856B-13
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SIGNAL
LOCATION: (1)..(28)
OTHER INFORMATION:
FEATURE:
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CITY: Boulder
US-09-570-856B-13
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US-08-315-695-21
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Sequence 3, Application 08/104445

Patent No. 5306633

GENERAL INFORMATION:
PAPLICANT: GOTTSCHALK, MICHAEL
APPLICANT: SPROBESIER, BRUNO
TITLE OF INVENTION: PRODUCTION, BACTERIA PRODUCING A XYLANASE, DNA FRAGMENT
TITLE OF INVENTION: BAKING AGENTS CONTAINING A XYLANASE, AND METHOD FO
NUMBER OF SEQUENCES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 VGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 VKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNAWKSHG 185
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Pred. No. 1.7e-95;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/104,445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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APPLICATION NUMBER: US/08/315,695
FILING DATE: 30-SEP-1994
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P.
REGISTATION NUMBER: 55-94
TELEFOND NUMBER: 55-94
TELEFHONE: (303) 499-8080
TELEFHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.5%;
Matches 207; Conservative
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                                                                                                                                                                                                                                                                                                                  208 amino acids
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                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                     linear
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STATE: Virginia
COUNTRY: U.S.A.
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TOPOLOGY: li
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96.5%; Score 1130; DB 1; Length 213;
Best Local Similarity 95.3%; Pred. No. 1.7e-94;
Matches 203; Conservative 4; Mismatches 6; Indels
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Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Ming L. Sung
APPLICANT: Mokoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: Robert L. Campbell
APPLICANT: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NIMBER OF SEVENTION: OF A LOW MOLECULAR MASS TALANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette, 5.25 in., 360kB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
                  NAME: Oblon, No. 5306633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 413-220
TELEEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
NOLECTUE TYPE: protein
US-08-104-445-3
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Errat
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5306633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-044-621D-37
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89 NGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTCTYKGTVKSDGGTYDIYTTTRYNAPSIDG 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 DRITFIQYWSVRQSKRPTGSNATITFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSS 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAP
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Patent No. 5759840

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Taguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatric, Cella, Harper, and Scinto STREET: 277 Park Ave.
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: Paice M.G., Bourbonnais R., Desrochers
AUTHORS: M., Jurasek L., & Yaguchi M.
                                                                                                                                                                                      STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                         ANTI-SENSE: No
PRAGMENT TYRE: No
ORIGINAL SOURCE:
ORGANISM: Bacillus subtilis
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE:
JOURNAL: Arch. Microbiol
                                                                    TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          DESCRIPTION: protein
                                                                                                                                                                   Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAGES: 201-206
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 185; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 NVTVW 213
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                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOLUME: 144
ISSUE:
                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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                                                                                                                                               LENGTH:
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Thermostability

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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG 120
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Sequence 5, Application US/09047370

Sequence 5, Application US/09047370

Patent No. 5866408

GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L

APPLICANT: Yaguchi Dr., Makoto

APPLICANT: Ishikawa Dr., Kazuhiko

TITLE OF INVENTION: Thermophilicity, Alkalophilicity and

TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr. Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE: (212) 758-2400
TELEPHONE: (212) 758-2400
TELEPHONE: (212) 758-2400
TELEPHONE: (212) 758-2400
TELEPHONE: (212) 758-2923
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acid
TYPE: amino acid
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: internal ORIGITMAL SOURCE: ORGANISM: Bacillus subtilus PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jurasek, L
Yaguchi, M
Arch. Microbiol.
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Desrochers, M
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Best Local Similarity 100.
Matches 185; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parce, M.G.
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|NVTVW 185
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; DATE: 1986
US-08-709-912-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
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AUTHORS:
AUTHORS:
AUTHORS:
AUTHORS:
JOURNAL:
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89 NGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG 148
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                                                                                                                                                                                                                                                                                                                                                                             COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
RILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: O18-M M. WARTEN E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
MEDIUM TOWNEY TOWNEY
                                                                                     ADDRESSEE: Fitzpatric, Cella, Harper, and Scinto STREET: 277 Park Ave.
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TELEFAX: (212) 758-2982
INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parce, M.G.
Bourbonnais, R
Desrochers, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Jurasek, L
AUTHORS: Yaguchi, M
JOURNAL: Arch. Micro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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ANTI-SENSE: NO
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Score 1038; DB 1; Length 185; Pred. No. 3e-86;
                                                                       APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Wang L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Mobert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette, 5.25 in., 360kB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yang R.C.A., MacKenzie C.R. & Narang
AUTHORS: R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION WABER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION NUMBER: BILING DATE:
FILING DATE: APPLICATION NUMBER: STORNEY/AGENT INFORMATION:
NAME: JUGY A. Errart
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECPHONE: 613-786-0199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 185
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
                 Sequence 36, Application US/08044621D Patent No. 5405769 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL: Nucleic Acids Res
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99.5%;
                                                                                                                                                                                                                                                                                                          CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 185
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: No
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ISSUE:
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-08-044-621D-36
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                                                                                                                           1 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAP
                                                                                     29 ASTDYWQNWIDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAP
    Gaps
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0
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APPLICANT: Suguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES:
ADDRESSEE: Fitzpatric, Cella, Harper, and Scinto
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,912

FILING DATE: 09-SEP-1996

CLESSIFFCATION: 435

ATTORNEY/AGENT INVERMATION:

NAME: 018en Mr. Warren E

REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 27290

TELEFRANCE/DOCKET NUMBER: 27200

TELEFRANCE/DOCKET NUMBER: 27200

TELEFRANCE/LOCKET NUMBER: 27200

TELEFRANCE/LOCKET NUMBER: 27200

TELEFRANCE/LOCKET NUMBER: 27200

TELEFRANCE/DOCKET NUM
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STREET: 277 Park Ave.
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: Yang, R.C.A.
AUTHORS: MacKenzie, C.R.
AUTHORS: Narang, S.A.
JOURNAL: Nucleic Acid Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
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ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORGANISM: Bacillus circulans
    Matches 184; Conservative
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STATE: New York
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NVTVW 213
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                                                                                         JOURNE: 16
VOLUME: 16
PAGES: 7187
ORGANISM:
PUBLICATION I
AUTHORS: Y
AUTHORS: M
AUTHORS: N
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US-09-570-856B-5
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                                                                                                                              29 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAP 88
                                                                                                                                                    1 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAP 60
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                                                     Query Match 88.6%; Score 1038; DB 1; Length 185; Best Local Similarity 99.5%; Pred. No. 3e-86; Matches 184; Conservative 1; Mismatches 0; Indels C
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APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatric, Cella, Harper, and Scinto STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
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ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: 01sen MY, Marren B
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE (212) 758-2940
TELEPHONE (212) 758-2940
TELEPAX: (212) 758-2942
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acids
TYPE: AMINOR SEG ID
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TOPOLOGY: linear
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US-08-709-912-3
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89 NGNGYLTLYGWTRSPLIEYYVVDSWCTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG 148
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Pred. No. 3e-86;
1; Mismatches 0; Indels (
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                                    Yang, R.C.A.
MacKenzie, C.R.
Narang, S.A.
Nucleic Acid Research
Bacillus circulans INFORMATION:
                                                                                                                                                                                                    Query Match 88.6%;
Best Local Similarity 99.5%;
Matches 184; Conservative
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89 NGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG 148
                                                                                                                                                                                       1 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFKTINFNAGWAP
                                                                                                            DRITTFIQYWSVRQSKRPIGSNATIIFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSS
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               ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAP
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GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahlyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: 105/09/570, 856B
CURRENT FILING DATE: 2002-04-15
PRIOR PILING DATE: 1999-05-12
MINDER OF FILING DATE: 1999-05-12
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APPLICANT: Bentzien, Joerg M
APPLICANT: Bentzien, Joerg M
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570, 8568
CURRENT FILING DATE: 2002-04-15
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SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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Matches 174; Conservative
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                                                                                                                        GENERAL INCORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Bentzien, Joerg M
APPLICANT: Bentzien, Joerg M
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASB
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR PILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 9
LENGTH: 185
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APPLICANT: Bentzien, Joerg M
APPLICANT: Bentzien, Joerg M
APPLICANT: Bentzien, Joerg M
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 185
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Pred. No. 6.5e-81;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 984; DB 2; Length 18
Pred. No. 2.3e-81;
6; Mismatches 6; Indels
                                                                                        Sequence 9, Application US/09570856B Patent No. 6682923
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Patent No. 6682923
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93.5%;
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Best Local Similarity 94.1%;
Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: synthetic US-09-570-856B-7
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Best Local Similarity 93.5'
Matches 173; Conservative
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| NVTVW 185
181 NVTVW 185
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                                                         RESULT 12
US-09-570-856B-9
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US-09-570-856B-7
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Search completed: February 3, 2006, 09:12:10 Job time : 29 secs

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US-10-517-939-188
                   TYPE: PRT
ORGANISM: Unknown
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311.993 Million cell updates/sec
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                                                                                                                               1 MFKFKKKNFLVGLSAALMSIS......YQVMATEGYQSSGSSNVTVW 213
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1: /cgnZ 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
2: /cgnZ 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
3: /cgnZ 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgnZ 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
5: /cgnZ 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
7: /cgnZ 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
7: /cgnZ 6/ptodata/2/pubpaa/USO1 NEW PUB.pep:*
8: /cgnZ 6/ptodata/2/pubpaa/USI1 NEW PUB.pep:*
8: /cgnZ 6/ptodata/2/pubpaa/USI1 NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-170-653-16
US-10-517-939-224
US-11-170-653-17
US-10-517-939-230
US-10-517-939-230
US-10-517-939-158
US-10-517-939-158
US-10-517-939-158
US-10-517-939-158
US-10-517-939-252
US-10-517-939-378
US-11-170-653-42
US-11-170-653-43
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Maximum Match 100%
Listing first 45 summaries
                                           protein search, using sw model
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US-11-170-653-40
US-11-108-163B-10
US-11-108-163B-14
US-11-108-163B-13
US-11-108-163B-13
US-11-170-653-39
US-11-170-653-39
US-11-170-653-38
US-11-170-939-236
US-10-517-939-256
US-10-517-939-156
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Sequence 188, Application US/10517939
; Publication No. US2006003433A1
; Publication No. US2006003433A1
; GREERAL INFORMYION:
; APPLICANT: Callen, Walter
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Beteghlalian, Alireza
; APPLICANT: Beteghlalian, Alireza
; TITLE OF INVENTION: AND METHOOS FOR MAKING AND USING THEM
; TITLE OF INVENTION: AND METHOOS FOR MAKING AND USING THEM
; TITLE OF INVENTION: AND METHOOS FOR MAKING AND USING THEM
; FILE REFERENCE: 56462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT PLING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR APPLICATION NUMBER: 60/389,299
; RINGR APPLICATION NUMBER: 60/389,299
; RINGR APPLICATION NUMBER: 60/389,299
; NUMBER OF SEQ 1D NOS: 380
; SOFTWARE: PastSEQ for Windows Version 4.0
; LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 213;
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APPLICANT: Sibbsen, Ole
APPLICANT: Scremen, Jens
TITLE OP INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanse Inhibitor
TITLE OP INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanse Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT PILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATCHIL VETSION 3.0
SEQ ID NO 17
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 1168; DB 6;
Pred. No. 1.4e-95;
1; Mismatches 0;
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Pred. No. 1.4e-95;
1; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOPTWARE: FastSEQ for Windows Version 4.0
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/11170653 Publication No. US20050271769A1 GENERAL INFORMATION: APPLICANT: Danisco A/S
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Best Local Similarity 99.5%;
Matches 212; Conservative
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Best Local Similarity 99.5%;
Matches 212; Conservative
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                                                                                                                                                                                                                                                                                                            ; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-224
                                                                                                                                                                                                TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-170-653-17
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                                                                                                                                                                                                                                                          GENERAL INPORMATION:
APPLICANT: Sibbean, Ole
APPLICANT: Sibbean, Ole
APPLICANT: Scrensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REPERENCE: 674509-203
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT TILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR PILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 16
LENGTH: 213
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Squence 224, Application US/10517939

Publication No. US20060003433A1

GENERAL INFORMATION:

APPLICANT: Scalen, Walter

APPLICANT: Healey, Shaun

APPLICANT: Hazlewood, Geoff

APPLICANT: Wu, Di

APPLICANT: Blum, David

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM

FILE REFERENCES: 564462007901

CURRENT APPLICATION UNMBER: US/10/517,939
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Best Local Similarity 100.0%; Pred. No. 7.6e-96;
Matches 213; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVW 213
                                                                                    181 WKSHGMNLGSNWAYQVMATEGYQSGSSNVTVW 213
                                                       181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
                                                                                                                                                                                                                      Sequence 16, Application US/11170653
Publifation No. US20050271769A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Bacillus subtilis
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                        61 TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPIG 120
                                                                                           TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
                                                                                                                   61 TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
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TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Scient, Malter
APPLICANT: Acallen, Malter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Blum, David
APPLICANT: Blum, David
APPLICANT: Blum, David
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
94.3%; Score 1104; DB 6; Length 213;
Best Local Similarity 93.0%; Pred. No. 5.5e-90;
Matches 198; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Obtained from an environmental sample
                                                                                                                                                                                  181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                                                                                                                                                                                                           Sequence 230, Application US/10517939
Publication No. US20060003433A1
GENERAL INFORMATION:
APPLICANT: Steer, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-230
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ORGANISM: Unknown
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Sequence 302, Application US/10517939 Publication No. US20060003433A1

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Sequence 1, Application US/11170653

Sequence 1, Application US/11170653

Sequence 1, Application Wo. US20050271769A1

GENERAL INFORMATION:
APPLICANT: Dains co A/S

APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
ITLE OF INVERTION: Xylanse Variants Having Altered Sensitivity to Xylanse Inhibitor
FILE REFERENCE: 674509-2046
CURRENT FILING DATE: 2005-66-23
FILE REPERENCE: 2005-66-23
FRIOR APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-03-08
PRIOR PELING DATE: 2000-03-08
PRIOR PELING DATE: 2000-03-08
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0
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JOURDAYL INFORMATION:
JAPPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: Hazlewood, Geoff
APPLICANT: Hazlewood, Geoff
APPLICANT: Hu, Di
APPLICANT: But But But But But But Barbil Barbil Barbil APPLICANT: Beteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: 2004-12-13
CURRENT APPLICATION NUMBER: US/10/517, 939
CURRENT PILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
TARAGET STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.7%; Score 1097; DB 6; Length 213; 92.0%; Pred. No. 2.3e-89; vative 10; Mismatches 7; Indels
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OTHER INFORMATION: Obtained from an environmental sample.
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Best Local Similarity 92.0*
Matches 196; Conservative
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NAME/KEY: SIGNAL

LOCATION: (1) ... (28)

US-10-517-939-302
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ORGANISM: Unknown
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RESULT 10
US-11-170-653-19
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                                                                                                                                                                                                                                                                                                                                                                                                    121 DRITFTQYWSVRQSKRPIGSNAIIFSNHVNAWKSHGMNLGSNWAYQVWATEGYQSGSS 180
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                                                                                                                                                                                                                                                                                               99 NGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG 148
                                                                                                                                                                                                               29 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAP 88
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Sequence 198, Application US/10517939

Publication No. US20060003433A1

GENERAL INFORMATION:

APPLICANT: Scaler, Malter

APPLICANT: Healey, Shaun

APPLICANT: Healey, Shaun

APPLICANT: Healey, Shaun

APPLICANT: Hazlewood, Geoff

APPLICANT: Hazlewood, Geoff

APPLICANT: Mu, Di

APPLICANT: Blum, David

APPLICANT: Wu, Di

BRIOR APPLICATION NUMBER: PCT/US03/19153

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14
                                                                                                                           Query Match 88.9%; Score 1041; DB 7; Length 185; Best Local Similarity 100.0%; Pred. No. 1.5e-84; Matches 185; Conservative 0; Mismatches 0; Indels (
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81.7%; Pred. No. 9e-77;
ive 13; Mismatches 24; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 198
LENGTH: 211
; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
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US-10-517-939-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVTVW 213
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: SIGNAL
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Best Local Simil
Matches 174; C
                                                                                      US-11-170-653-1
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Sequence 19, Application US/11170653
; Publication No. US20050271769A1
; Publication No. US20050271769A1
; Publicant INFORMATION:
APPLICANT: Danisco A/S
; APPLICANT: Stabbesen, Ole
; APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
120 TYKGTVTSDGGTYDIYTTWRHNAPSIDGTQ-TFAQYWSVRQSKRATGVNSSITFSNHVNA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 NTGNEVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVROSKRPTGSNATITFSNHVN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MFKFKKNFLVGLSAALMS-ISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWS
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                                                                                                                                                                                                                                                                                                                                                                             STOREAGN INFOGRATION:

APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Hu, Di
APPLICANT: Hu, Di
APPLICANT: Blum, David
APPLICANT: BLUM, DAVID
APPLICANT: BLUM, DAVID
APPLICANT: BLOOM NAMES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAXING AND USING THEM
TITLE OF INVENTION: AND METHODS FOR MAXING AND USING THEM
TITLE OF INVENTION NUMBER: US/10/517,939
CURRENT APPLICATION NUMBER: US/10/517,939
FRIOR PLILING DATE: 2003-06-16
PRIOR PELING DATE: 2003-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE FREEED for Windows Version 4.0
SEQ ID NO 158
LENGTH: 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.7%; Score 933.5; DB 6; Best Local Similarity 80.4%; Pred. No. 4.6e-75; Matches 172; Conservative 12; Mismatches 29;
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                                                                                       181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
                                                                                                                   179 WASKGMNLGSSWSYQVIATEGYQSSGSSNVTVW 211
                                                                                                                                                                                                                                                                                            Sequence 158, Application US/10517939; Publication No. US20060003433A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: SIGNAL
; LOCATION: (1)...(29)
US-10-517-939-158
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RESULT 13
US-10-517-939-190
                                  Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 TGNFVVGKGWTYGTPNRVVNYNAGVPAPSGNGYLTFYGWTRNALIEYYVVDSWGTYRPTG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 TYKGTVNSDGGTYDIYTTMRYNAPSIDGTQ-TPPQYWSVRQSKRPTGVNSTITFSNHVNA 178
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Sequence 208, Application US/10517939
Sequence 208, Application US/10517939
Sequence 208, Application US/20060003433A1
GENERAL INFORMATION:
APPLICANT: Scaler, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Blum, David
APPLICANT: Blum, David
APPLICANT: Blum, David
ITILE OF INVENTION: XTHANDSE, NUCLEIC ACIDS ENCODING THEM
ITILE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
ITILE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
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TILE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
STORRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/389, 299
PRIOR FILING DATE: 2002-06-14
NUMBER: OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 208
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%; Score 929; DB 7; Length 211; 79.3%; Pred. No. 1.1e-74; Live 18; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Obtained from an environmental sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR FILING DATE: 2002-09-09

PRIOR PILING DATE: 2001-03-08

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 19

LENGTH: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 169; Conservative
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', NAME/KEY: SIGNAL

; LOCATION: (1)...(27)

US-10-517-939-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: A. caviae
US-11-170-653-19
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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Best Local 9
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JERNEAL INFORMATION
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JERNET SIDDESEN, Ole
JAPPLICANT: Stobesen, Ole
JAPPLICANT: Stobesen, Ole
JAPPLICANT: Stobesen, Ole
JELE APPLICANT: Storensen, Jens
JELE APPLICANT: Storensen, Jens
JELE REFERENCE: 674509-2046
JELE REFERENCE: 674509-2046
JELE REFERENCE: 674509-604
JELE REFERENCE: 0002-09-09
JERICA PAPLICATION NUMBER: US/10/237,386
JERICA PRILING DATE: 2001-03-08
JERICA PAPLICATION NUMBER: GB 0005585.5
JERICA APPLICATION NUMBER: GB 0005585.5
JERICA APPLICATION NUMBER: GB 0015751.1
JERICA APPLICATION NUMBER: GB 0015751.1
JERICA PAPLICATION NUMBER: GB 0015751.1
JERICA APPLICATION NUMBER: GB 0015751.1
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                                                                                                                                                                                                                                                                                                                                   61 NFVVGKGWSVGSPNRTINYNAGIWEPSGNGYLTLYGWTRNSLIEYYVVDSWGTYRPTGTH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    123 KGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNAWK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KGIVNSDGGTYDIYITHRYNAPSIDGTQ-TFQQFWSVRQSKRPTGSNVSITFSNHVNAMR 179
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                                                                              Gaps
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ب
   Length 210;
; Score 927; DB 6; Length 21; Pred. No. 1.7e-74; 14; Mismatches 26; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 KSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/11170653; Publication No. US20050271769A1; GENERAL INFORMATION:
       79.2%;
                                        Best Local Similarity 80.18 Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 168; Conservative
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US-11-170-653-18
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90 GNGYLTLYGWTRSPLIEYYVVDSWGTYRPIGTYKGTVKSDGGTYDIYTTTRYNAPSIDGD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 RITFIQYWSVRQSKRPTGSNATITFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPS 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GNGYLTLYGWTRNSLIEYYVVDSWGTYRPTGTHKGTVNSDGGTYDIYTTWRYNAPSIDGT 121
                                                                                                                                                                                                                                                                                                                                                                    2 AIDYWQYWIDGGGIVNAVNGSGGNYSVIWQNSGDFVVGKGWSVGSPNRIININAGIWEPS 61
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                                                                                                                                                                                                                                                                                                                                          30 STDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPN
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                                                                                                                                                                                                                           Length 184;
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APPLICANT: Steer, Walter
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Hazlewood, Geoff
APPLICANT: Balum, David
APPLICANT: Beteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 56462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FESTSER FOR WINGOWS Version 4.0
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                                                                                                                                                                                                                                                                               15; Indels
                                                                                                            ; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THER INFORMATION: Synthetically generated polypeptide
                                                                                                                                                                                                                     Query Match 74.6%; Score 873.5; DB 6; Best Local Similarity 83.2%; Pred. No. 7e-70; Matches 153; Conservative 15; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 380, Application US/10517939; Publication No. US20060003433A1; GENERAL INFORMATION:
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Matches 153; Conserv
SEQ ID NO 252
LENGTH: 184
TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 VTVW 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 FSPSGNGYLALYGWTRNSLIEYYVVDSWGTYRPTGTYKGTVTSDGGTYDIYTTTRTNAPS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 IDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNAWKSHGMNLGSNWAYQVMATEGYQSS 205
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                                                                                                APPLICANT: Scient Watter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healewood, Geoff
APPLICANT: Hallan, David
APPLICANT: Blum, David
APPLICANT: Blum, David
TITLE OF INVENTION: XYLANASE, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
CURRENT APPLICATION NUMBER: DCT/US03/19153
PRIOR FILING DATE: 2004-12-13
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 190
LENGTH: 189
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Sequence 252, Application US/10517939

Publication No. US20060003433A1

Semeral Information:
APPLICANT: Steer, Brian
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Hazlewood, Geoff
APPLICANT: Blum, David
APPLICANT: Blum, David
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
TITLE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2003-06-16
PRIOR PILING DATE: 2003-06-16
PRIOR PILING DATE: 2003-06-16
PRIOR PILING DATE: 2003-06-16
NUMBER OF SEQ ID NOS: 380

SOFTWARE: FastSEQ for Mindows Version 4.0
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Sequence 190, Application US/10517939
Publication No. Us20060003433A1
GENERAL INFORMATION:
APPLICANT: Steer, Brian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Unknown
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206 GSSNVTVW 213 | |||||| 182 GYSNVTVW 189

Search completed: February 3, 2006, 09:13:20 Job time : 8 secs

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Sequence 11,
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1 MFKFKKNFLVGLSAALMSIS......YQVMATEGYQSSGSSNVTVW
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/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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US-10-626-724-7

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US-10-626-724-9

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GenCore version
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Sequence 16, Application US/10237386

; Sequence 16, Application US/10237386
; Sequence 16, Application US/10237386
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sibbesen, Ole
; TILE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
; TILE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
; TILE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT FALING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
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US-10-237-386-43
US-10-237-386-42
US-10-237-386-41
US-10-237-386-41
US-10-307-441-13
US-10-307-441-13
US-10-286-993-2
US-10-286-993-2
US-10-286-993-2
US-10-237-386-39
US-10-237-386-39
US-10-237-386-39
US-10-237-386-39
US-10-237-386-39
US-10-237-386-39
US-10-237-386-39
US-10-307-441-10
US-11-088-725A-38
US-10-307-441-10
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US-10-307-441-10
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US-10-626-583-5
; Sequence 5, Application US/10626583
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   US-10-237-386-16
  SEQ ID NO 16
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US-11-018-645-8 US-11-018-645-16 US-11-018-645-4 US-11-018-645-4

Sequence Sequence

Sequence

Sequence Sequence

Sequence

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Publication No. US20040234998A1
GENERAL INPORMATION:
APPLICANT: SIBBESEN, OLE
FAPLICANT: SIBBESEN, OLE
FILE REPERENCE: 078837013.
FILE REPERENCE: 078837013.
CURRENT APPLICATION NUMBER: US/10/626,583
CURRENT FILING DATE: 2003-07-25
PRIOR PELING DATE: 2001-01
PRIOR PELING DATE: 2001-10-01
PRIOR PILING DATE: 1999-12-17
PRIOR PILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-3
PRIOR FILING DATE: 1998-12-3
PRIOR FILING DATE: 1999-04-06
PRIOR PILING DATE: 1999-04-06
PRIOR PILING DATE: 1999-04-05
PRIOR PILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SEQ ID NO S: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-626-583-5
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1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN Gaps 0; Indels 100.0%; Score 1171; DB 5; 100.0%; Pred. No. 1.5e-96; tive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 213; Conservative

61 TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120 TGNFVVGKGWTTGSPFRIINYNAGVWAPNGNGYLTLYGWTRSPLIEXYVVDSWGTYRPIG 120 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180 1 MFKFKKNFLVGLSAALMSISLFSATASAASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSN 60 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213 121 음 ò å 셤 8 ઠે

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US-110-26-7(24-2):
Sequence 5. Application US/10626724
Publication No. US20050079573A1
GENERAL INFORMATION:
APPLICANT: SIBBESEN, OLE
APPLICANT: SORENSEN, JENS FRISBAEK
TITLE OF INVENTION: PROTEINS
FILE REPERENCE: 078883/0132
CURRENT APPLICATION NUMBER: US/10/626,724
CURRENT PILING DATE: 2003-07-25
PRIOR PILING DATE: 2001-06-25
PRIOR PILING DATE: 1999-12-17
PRIOR PILING DATE: 1999-12-17
PRIOR PILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-04-06
PRIOR PILING DATE: 1999-04-06
PRIOR PILING DATE: 1999-04-15
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Sequence 17, Application US/10237386;
Publication NO US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Stobesen, Ole
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/1B01/00426
PRIOR APPLICATION NUMBER: PCT/1B01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
SPRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
SPRIOR PAPILCATION NUMBER: GB SPRIOR DATE: 2000-06-27
SPRIOR PAPILCATION NUMBER: GB SPRIOR DATE: 2000-06-27
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Pred. No. 1.5e-96;
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                                                                                            Query Match 100.0%; Score 1171; Best Local Similarity 100.0%; Pred. No. 1.5 Matches 213; Conservative 0; Mismatches
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; ORGANISM: Bacillus circulans
US-10-237-386-17
; ORGANISM: Bacillus subtilis
US-10-626-724-5
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RESULT 5 US-10-626-583-11

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SOFTWARE: Patentin Ver. 2.1
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Mutant Xylanase
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99.1%; Score 1161; DB 5;
Best Local Similarity 99.1%; Pred. No. 1.2e-95;
Matches 211; Conservative 0; Mismatches 2;
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Sequence 11, Application US/10626583
Publication No. US20040234998A1
GENERAL INFORMATION:
APPLICANT: SIBBESRN, OLE
APPLICANT: SORENSEN, JENS FRISBAEK
TITLE REFERENCE: 078883/0132
CURRENT APPLICATION NUMBER: US/10/626,583
CURRENT FILING DATE: 2003-07-25
PRIOR PLING DATE: 2001-10-01
PRIOR PLING DATE: 1999-12-17
PRIOR PLING DATE: 1999-12-17
PRIOR PLING DATE: 1999-12-17
PRIOR PLING DATE: 1999-12-17
PRIOR PLING DATE: 1998-12-17
PRIOR PLING DATE: 1998-12-17
PRIOR PLING DATE: 1998-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PARENT NOWER: 21
SOFTWARE: PARENT NOWER: 21
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STRBESEN, OLE
APPLICANT: SORENSEN, JENS FRISBAEK
TITLE OF INVENTION: PROTEINS
FILE REPERENCE: 070883/0132
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US/09/869,155
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: PCT/1B99/02071
PRIOR APPLICATION NUMBER: GB 9828599.2
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: GB 9907805.7
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: GB 9907805.7
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
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ORGANISM: Artificial Sequence
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US-10-626-724-11
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                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Mutant Xylanase US-10-626-724-11
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                                                                                                                                                                                        Length 213;
                                                                                                                                                                                  Score 1161; DB 5; Length 2
Pred. No. 1.2e-95;
0; Mismatches 2; Indels
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Publication No. US20040234998A1

GENERAL INFORMATION:

APPLICANT: SIBENESN, OLE

APPLICANT: SORENSEN, JENS FRISBAEK

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: 078883/0132

CURRENT FILING DATE: 2003-07-25

PRIOR APPLICATION NUMBER: US/09/869,155

PRIOR PLING DATE: 2001-10-01

PRIOR FILING DATE: 1999-12-17

PRIOR PLING DATE: 1999-12-17

PRIOR PLING DATE: 1999-12-23

PRIOR PLING DATE: 1999-12-23

PRIOR PLING DATE: 1999-04-06

PRIOR FILING DATE: 1999-04-06

PRIOR FILING DATE: 1999-04-15
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Best Local Similarity 99.1%;
Matches 211; Conservative
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TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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Best Local Similarity 98.1
Matches 209; Conservative
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61 TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
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Sequence 9, Application US/10626724
PUDLICACION NO. US20050079573A1
GENERAL INFORMATION:
APPLICANT: SIBBESEN, OLE
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 078891/0125
CURRENT APPLICATION NUMBER: US/10/626,724
CURRENT APPLICATION NUMBER: US/09/869,155
PRIOR APPLICATION NUMBER: PCT/IB99/02071
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-3
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 9
LENGTH: 213
CURRENT APPLICATION NUMBER: US/10/626,583
CURRENT FILING DATE: 2003-07-25
PRIOR PELICATION NUMBER: US/09/869,155
PRIOR FILING DATE: 2001-10-01
PRIOR FLING DATE: 1999-12-17
PRIOR FLING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: GB 9908645.6
PRIOR PILING DATE: 1999-04-06
PRIOR PILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 9
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ORGANISM: Artificial Sequence
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           61 TGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.5%; Score 1154; DB 5; Length 213; Best Local Similarity 98.1%; Pred. No. 4.9e-95; Matches 209; Conservative 2; Mismatches 2; Indels
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APPLICANT: SORENSEN, JENS FRISBAEK
TITLE OF INVENTION: PROTEINS
FILE REPERRUE: 078883/0132
CURRENT APPLICATION NUMBER: US/10/626,724
CURRENT FILING DATE: 2003-07-25
PRIOR PILING DATE: 2001-06-25
PRIOR PLING DATE: 1999-12-17
PRIOR PLING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR PLING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.1
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Sequence 9, Application US/10626583

Publication No. US20040234998A1

GUBERAL INFORMATION:
APPLICANT: SIBBESEN, OLE
APPLICANT: SORENSEN, JENS FRISBAEK
TITLE OF INVENTION: PROTEINS
FILE REPERENCE: 078883/0132
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Publication No. US20050079573A1
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ORGANISM: Artificial Sequence
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APPLICANT: SUNG, Wing L.
APPLICANT: SUNG, Wing L.
APPLICANT: SUNG, Wing L.
APPLICANT: SUNG, Wing L.
TITLE OF INVENTION: Modified Xylanaese Exhibiting Increased Thermophilicity
TITLE OF INVENTION: and Alkalophilicity
FILE REFERENCE: 027367-5006US
CURRENT APPLICATION NUMBER: US/10/307,441
PRIOR APPLICATION NUMBER: PCT/CA01/00769
PRIOR PLING DATE: 2001-05-31
PRIOR PLING DATE: 2001-05-31
PRIOR FILING DATE: 2001-05-31
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US-10-626-724-3
181 WKSHGMNLGSNWAYQVLATEGYKSSGSSNVTVW 213
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                                                                                                                                                                                       GENERAL INFOCANT: STREESEN, OLE
APPLICANT: STREESEN, OLE
APPLICANT: STREESEN, JENS FRISBAEK
TITLE OF INVENTION: PROTEINS
CURRENT APPLICATION NUMBER: US/10/626,724
CURRENT FILING DATE: 2003-07-25
PRIOR PLING DATE: 2003-07-25
PRIOR PLING DATE: 1999-12-17
PRIOR PLING DATE: 1999-12-17
PRIOR FLING DATE: 1999-12-17
PRIOR FLING DATE: 1999-12-3
PRIOR FLING DATE: 1999-12-3
PRIOR FILING DATE: 1999-12-3
PRIOR FILING DATE: 1999-12-3
PRIOR FILING DATE: 1999-12-3
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SEQ ID NOS: 19
                                                                                                                        ; Sequence 3, Application US/10626724; Publication No. US20050079573A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10307441 Publication No. US20030166236A1 GENERAL INFORMATION:
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ORGANISM: Unknown Organism
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Matches 203; Conservative
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US-10-626-583-3
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                                                                         Query Match
98.1%; Score 1149; DB 5;
Best Local Similarity 97.7%; Pred. No. 1.4e-94;
Matches 208; Conservative 2; Mismatches 3;
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APPLICANT: SCRENSEN, OLE
APPLICANT: SCRENSEN, JENS FRISBAEK
TITLE OF INVENTION: PROTEINS
CURRENT APPLICATION NUMBER: US/10/626,583
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US/09/869,155
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: GB 9828599.2
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: GB 9907805.7
PRIOR APPLICATION NUMBER: GB 9908645.6
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19

; OTHER INFORMATION: Mutant Xylanase
US-10-626-724-9
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Publication No. US20040234998A1
GENERAL INFORMATION:
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ORGANISM: Unknown Organism
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LENGTH: 213
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89 NGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG 148
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APPLICANT: White, Theresa C
APPLICANT: White, Theresa C
APPLICANT: White, Theresa C
APPLICANT: Wallace, Katie E.A.
TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
CURRENT APPLICATION WHERE: US/11/089,725A
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/556,061
PRIOR APPLICATION NUMBER: US 60/556,061
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Version 3.2
SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.9%; Score 1041; DB 6; Best Local Similarity 100.0%; Pred. No. 5.3e-85; Matches 185; Conservative 0; Mismatches 0;
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                                                             Sequence 32, Application US/11088725A
Publication No. US20050214410A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Bacillus subtilus
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| GENERAL INFORMATION:
| APPLICANT: Danisco A/S
| APPLICANT: Sibbesen, Ole
| APPLICANT: Soremsen, Jense
| TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanse Inhibitor
| FILE REFERENCE: 674509-2046
| CURRENT APPLICATION NUMBER: US/10/237,386
| CURRENT FILING DATE: 2002-12-06
| PRIOR FILING DATE: 2001-03-08
| PRIOR FILING DATE: 2000-03-08
| SPRIOR FILING DATE: 2000-03-08
| SOFTWARE: Patentin version 3.0
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                                                                                                                                 Query Match 88.9%; Score 1041; DB 4; Length 185; Best Local Similarity 100.0%; Pred. No. 5.3e-85; Matches 185; Conservative 0; Mismatches 0; Indels (
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                       ; LENGTH: 185
; TYPE: PT
; ORGANISM: Bacillus subtilis
US-10-307-441-5
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